

CC receptor-competent LDL particles do not require the complete apo B
CC sequence, which is large and tends to aggregate, to provide binding
XX affinity to an apo B protein receptor
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 63; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAEYKKNKRRH 11
DB 1 KAEYKKNKRRH 11

RESULT 2
ABJ37574
ID ABJ37574 standard; peptide; 16 AA.
XX
AC ABJ37574;
XX
DT 10-MAY-2003 (first entry)
XX
DE Heparin binding peptide sequence #27.
XX
KW Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW cardiovascular; circulatory; ligand; sulphated; sulphonated; tumour;
XX rheumatoid arthritis; hypoxia; diabetic retinopathy; heparin.
XX
OS Unidentified.
XX
PN WO2003007689-A2.
XX
PD 30-JAN-2003.
XX
PF 22-JUL-2002; 2002WO-US023419.
XX
PR 20-JUL-2001; 2001US-0306726P.
XX
PA (ETHZ-) ETH ZURICH.
XX (UYZU-) UNIV ZURICH.
XX
PI Hubbell JA, Schoenmakers R, Maynard HD;
XX WPI; 2003-300420/29.
XX
DR WPI; 2003-300420/29.
XX
PT Use of a ligand comprising of at least one sulfated or sulfonated amino
XX acid for the treatment of e.g. tumors, rheumatoid arthritis, diabetic
XX retinopathy and hypoxia.
XX
PS Disclosure; Fig 2; 79pp; English.
XX
CC The invention relates to a novel ligand for binding a target biomolecule,
XX which comprises a peptide having at least one sulphated or sulphonated
XX amino acid and at least one amino acid chosen from neutral and positively
XX charged amino acids. The novel ligands can be used for the treatment of
XX e.g. tumors, rheumatoid arthritis, diabetic retinopathy and hypoxia.
XX
CC This sequence represents a heparin binding peptide relating to the
XX invention.

Sequence 16 AA;
SQ

Query Match 95.2%; Score 60; DB 6; Length 15;
Best Local Similarity 90.9%; Pred. No. 0.00078;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAEYKKNKRRH 11
DB 4 KAEYKKNKRRH 14

RESULT 3
AAE14542

ID AAE14542 standard; peptide; 20 AA.
XX
AC AAE14542;
XX
DT 17-MAY-2002 (first entry)
XX
DE Human apob-100 derived peptide p63.
XX
KW Oxidised low density lipoprotein; oxLDL; immunoassay; periaortitis;
KW cardiovascular disease; coronary heart disease; pre-eclampsia;
XX peptide p63.
XX
OS Homo sapiens.
XX
PN WO200206314-A2.
XX
PD 24-JAN-2002.
XX
PF 18-JUL-2001; 2001WO-GB003212.
XX
PR 18-JUL-2000; 2000GB-00017641.
XX (ARKT-) ARK THERAPEUTICS LTD.
XX
PI Narayan O, Yla-Herttuala S;
XX WPI; 2002-179777/23.
XX
DR WPI; 2002-179777/23.
XX
PT New peptide useful in enzyme immunoassays for detecting oxidized low
XX density lipoprotein which is a marker of coronary heart disease and other
XX cardiovascular diseases, has affinity for oxidized low density
XX lipoprotein.
XX
PS Claim 6; Page 5; 21pp; English.
XX
CC The invention relates to peptides having affinity for oxidised low
XX density lipoprotein (oxLDL), in cyclised or multimeric form. The peptide
XX is useful in an immunoassay to determine the presence, and optionally,
XX the amount of antibodies in a sample, having affinity for oxLDL.
XX Preferably immobilised peptide is useful for measuring the amount of
XX autoantibodies for oxLDL in a sample, especially a serum or plasma sample
XX from a patient for evaluating the risk of coronary heart diseases, other
XX cardiovascular diseases, and several other disorders such as
XX periaortitis pre-eclampsia, non-insulin-dependent diabetes and
XX endothelial dysfunction. The peptide of the invention is stable, can be
XX synthesised easily without the need to isolate proteins from a patient's
XX blood, and has a long half-life. The present sequence is human apob-100
XX derived peptide p63 used in the invention
XX
SQ Sequence 20 AA;

Query Match 95.2%; Score 60; DB 5; Length 20;
Best Local Similarity 90.9%; Pred. No. 0.00099;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAEYKKNKRRH 11
DB 4 KAEYKKNKRRH 14

RESULT 4
AAE14545
ID AAE14545 standard; peptide; 24 AA.
XX
AC AAE14545;
XX
DT 17-MAY-2002 (first entry)
XX
DE Human apob-100 derived peptide p244.
XX
KW Oxidised low density lipoprotein; oxLDL; immunoassay; periaortitis;
KW cardiovascular disease; coronary heart disease; pre-eclampsia;
XX

Human apob-100 derived peptide p244.
KW Oxidised low density lipoprotein; oxLDL; immunoassay; periaortitis;
KW cardiovascular disease; coronary heart disease; pre-eclampsia;
XX

KW non-insulin-dependent diabetes; endothelial dysfunction; human; apob-100;
 KW peptide p244.
 XX
 OS Homo sapiens.
 XX
 PN WO200206314-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 18-JUL-2001; 2001WO-GB003212.
 XX
 PR 18-JUL-2000; 2000GB-00017641.
 XX
 PA (ARKT-) ARK THERAPEUTICS LTD.
 PI Narvanen O, Yla-Herttuala S;
 DR WPI; 2002-179777/23.
 XX
 PT New peptide useful in enzyme immunoassays for detecting oxidized low
 PT density lipoprotein which is a marker of coronary heart disease and other
 PT cardiovascular diseases, has affinity for oxidized low density
 PT lipoprotein.
 XX
 PS Claim 7; Page 21; 21pp; English.
 XX
 CC The invention relates to peptides having affinity for oxidised low
 CC density lipoprotein (oxLDL), in cyclised or multimeric form. The peptide
 CC is useful in an immunoassay to determine the presence, and optionally,
 CC the amount of antibodies in a sample, having affinity for oxLDL.
 CC Preferably immobilised peptide is useful for measuring the amount of
 CC autoantibodies for oxLDL in a sample, especially a serum or plasma sample
 CC from a patient for evaluating the risk of coronary heart diseases, other
 CC cardiovascular diseases, and several other disorders such as
 CC periaortitis, pre-eclampsia, non-insulin-dependent diabetes and
 CC endothelial dysfunction. The peptide of the invention is stable, can be
 CC synthesised easily without the need to isolate proteins from a patient's
 CC blood, and has a long half-life. The present sequence is human apob-100
 CC derived peptide p244 used in the invention
 CC
 SQ Sequence 24 AA;
 QY
 DB 1 KAEYKKNKGRH 11
 6 KAOYKKNKGRH 16
 RESULT 5
 AAM96844
 ID AAM96844 standard; peptide; 50 AA.
 XX
 AC AAM96844;
 XX
 DT 22-APR-1999 (first entry)
 XX
 DE Nucleic acid binding domain from apob-100.
 XX
 KW Human apolipoprotein B-100; apob-100; very-low density lipoprotein; VLDL;
 KW apolipoprotein; binding; in vivo transport; nucleic acid; binding domain;
 KW nuclear localisation sequence; gene therapy; cancer; cystic fibrosis;
 KW non-small cell lung carcinoma; diabetes; arteriosclerosis.
 XX
 OS Homo sapiens.
 XX
 PN WO9856938-A1.
 XX
 PD 17-DEC-1998.
 XX
 PF 10-JUN-1998; 98WO-US011977.

XX
 PR 13-JUN-1997; 97US-00874807.
 PR 14-MAY-1998; 98US-00079030.
 XX
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX
 PI Guevara JG, Hoogveen RC, Moore JP;
 DR WPI; 1999-070331/06.
 XX
 PT Composition comprising nucleic acid bound to LDL or VLDL lipoprotein -
 PT used for delivering nucleic acid to cells for gene therapy and antisense
 PT treatment.
 XX
 PS Claim 16; Page 150-151; 293pp; English.
 XX
 CC AAM96827-77 represent nucleic acid binding domains derived from human
 CC apolipoprotein B-100 (apob-100). Apob-100 is a major apoprotein component
 CC of very-low density lipoproteins (VLDL), intermediate density lipoprotein
 CC (IDL), low density lipoproteins (LDL) and lipoprotein a. The present
 CC sequence can be used in the composition of the invention. The
 CC specification describes a composition that comprises LDL and
 CC apolipoproteins for the binding and in vivo transport of nucleic acids.
 CC The composition is used to deliver nucleic acids to eukaryotic cells, in
 CC vivo or in vitro, for expressing a therapeutic polypeptide or antisense
 CC molecule (or ribozyme). Specifically they are used for gene therapy of
 CC cancers (particularly non-small cell lung carcinoma), diabetes, cystic
 CC fibrosis and arteriosclerosis
 CC
 SQ Sequence 50 AA;
 QY
 DB 1 KAEYKKNKGRH 11
 2 KAOYKKNKGRH 12
 RESULT 6
 AAM41259
 ID AAM41259 standard; peptide; 138 AA.
 XX
 AC AAM41259;
 XX
 DT 19-MAY-1998 (first entry)
 XX
 DE Apolipoprotein B-100 fragment.
 XX
 KW Anti-coagulant; apolipoprotein B-100; apob-100; metastatic spread;
 KW thromboplastin-mediated process; cancer; inhibitor; blood coagulation;
 KW angiogenesis; cellular differentiation; apoptosis; KRAD-14;
 KW prothrombinase complex.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9743311-A1.
 XX
 PD 20-NOV-1997.
 XX
 PF 09-MAY-1997; 97WO-GB001255.
 XX
 PR 09-MAY-1996; 96GB-00009702.
 XX
 PA (UNLO) ROYAL FREE HOSPITAL SCHOOL MED.
 XX
 PI Bruckdorfer KR, Ectelate C;
 XX
 DR WPI; 1998-008798/01.
 XX
 PT Peptide fragments of apo.lipo:protein B-100 with anticoagulant activity -

PT used for treating or preventing coagulation, inhibiting angiogenesis,
 PT cell differentiation and apoptosis.
 PS Claim 2; Page 8; 60pp; English.

CC This sequence is an example of the peptide of the invention. It has the
 CC formula (1), or their variants with one or more internal deletions,
 CC insertions or substitutions while retaining anti-coagulant properties,
 CC apolipoprotein B-100 (apob-100). 21-KAQ-XI-KKKKRRS-X2-1-42 (I) X1 = S or
 CC Y; X2 = T or I; Z1 = the N terminus of the peptide, a terminal amide group or 1-77
 CC aa. Compositions containing the peptide are used for simultaneous,
 CC separate or sequential treatment of cancer, particularly to prevent
 CC metastatic spread. They are also used to inhibit thromboplastic-mediated
 CC processes, specifically to prevent or reduce blood coagulation (e.g.
 CC during or after surgery or in cases of heart attack, stroke etc.) and to
 CC inhibit angiogenesis, cellular differentiation or apoptosis, KRAV-14, and
 CC which is active as such or as part of a 98-aa peptide, inhibits
 CC activation of the prothrombinase complex, and prevents activation of
 CC factor VII on the surface of thromboplastin and of platelets by thrombin.
 CC It binds to the residues 58-66 of thromboplastin and of platelets by thrombin.
 CC smaller than apob-100, they act more quickly
 XX Sequence 138 AA;

Query Match Best Local Similarity 95.2%; Score 60; DB 2; Length 138;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 1 KAEYKKKKRRH 11
 ||:|||||
 48 KAYKKKKRRH 58

RESULT 7
 AAW96831 standard; peptide; 394 AA.

AC AAW96831;
 XX
 DT 22-APR-1999 (first entry)

DE Nucleic acid binding domain from apob-100, residues 2930-3324.

KW Human apolipoprotein B-100; apob-100; Very-low density lipoprotein; VLDL;
 KW apolipoprotein; binding; in vivo transport; nucleic acid; binding domain;
 KW nuclear localisation sequence; gene therapy; cancer; cystic fibrosis;
 XX non-small cell lung carcinoma; diabetes; arteriosclerosis.

OS Homo sapiens.

XX
 PN WO9856938-A1.

PD 17-DEC-1998.

PF 10-JUN-1998; 98WO-US011927.

PR 13-JUN-1997; 97US-00874807.

PR 14-MAY-1998; 98US-00079030.

PA (BAYU) BAYLOR COLLEGE MEDICINE.

PI Guevara JG, Hoogveen RC, Moore JP;

DR WPI; 1999-070331/06.

PT Composition comprising nucleic acid bound to LDL or VLDL lipoprotein -
 PT used for delivering nucleic acid to cells for gene therapy and antisense
 PT treatment.

PS Claim 16; Page 144-145; 293pp; English.

XX AAW96827-77 represent nucleic acid binding domains derived from human

CC apolipoprotein B-100 (apob-100). Apob-100 is a major apoprotein component
 CC of very-low density lipoproteins (VLDL), intermediate density lipoprotein
 CC (IDL), low density lipoproteins (LDL) and lipoprotein a. The present
 CC sequence can be used in the composition of the invention. The present
 CC specification describes a composition that comprises LDL and
 CC apolipoproteins for the binding and in vivo transport of nucleic acids.
 CC The composition is used to deliver nucleic acids to eukaryotic cells, in
 CC vivo or in vitro, for expressing a therapeutic polypeptide or antisense
 CC molecule (or ribozyme). Specifically they are used for gene therapy of
 CC cancers (particularly non-small cell lung carcinoma), diabetes, cystic
 CC fibrosis and arteriosclerosis
 XX Sequence 394 AA;

Query Match Best Local Similarity 95.2%; Score 60; DB 2; Length 394;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 1 KAEYKKKKRRH 11
 ||:|||||
 218 KAYKKKKRRH 228

RESULT 8
 ADJ57400 standard; protein; 2463 AA.

AC ADJ57400;
 XX
 DT 06-MAY-2004 (first entry)

DE Human apolipoprotein B, marker for hepatocellular carcinoma.

KW Hepatocellular carcinoma; marker; human; apolipoprotein B; diagnosis.

XX Homo sapiens.

OS
 PN WO2004005466-A2.

PD 15-JAN-2004.

PF 03-JUL-2003; 2003WO-US020841.

PR 03-JUL-2002; 2002US-0393982P.

PA (ILLU-) ILLUMIGEN BIOSCIENCES INC.

PI Katze M, Bumgarner R, Smit M, Rosenberg G;

DR WPI; 2004-142977/14.

DR GENBANK; NP_000375.

PT Detecting hepatocellular carcinoma (HCC) in mammals comprises obtaining
 PT and assaying a biological sample to quantify a cell-associated or a non-
 PT cell-associated HCC-related protein and comparing the quantity to a
 PT control level.

PS Disclosure; SEQ ID NO 4; 48pp; English.

CC The present sequence is that of human apolipoprotein B. This non-cell
 CC associated protein is one of a set of proteins characterized as
 CC diagnostic targets for hepatocellular carcinoma (HCC). Such proteins are
 CC the products of genes identified by expression microarray analysis of
 CC tumour samples from hepatitis C virus (HCV) infected patients with HCC as
 CC being specifically up-regulated in HCC tumour tissue when compared to HCV
 CC infected cirrhotic non-tumour tissue and normal liver. The invention
 CC relates to the detection of HCC by assaying patient samples such as
 CC tissue, plasma, serum, etc. for the presence and level of specific HCC
 CC related proteins. A finding of elevated levels of one or more of these
 CC proteins in a patient sample indicates that the patient has HCC. Methods
 CC for the diagnosis of HCC are provided, as well as improved assay methods
 CC and scanning methods that employ non-cell-associated and cell-associated
 CC HCC-related proteins.

XX SQ Sequence 2463 AA;
Query Match 95.2%; Score 60; DB 8; Length 2463;
Best Local Similarity 90.9%; Pred. No. 0.16;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAEYKKNKRRH 11
DB 1074 KAQYKKNKRRH 1084
RESULT 9
AAAY31237
ID AAY31237 standard; protein, 3923 AA.
XX AAY31237;
XX AC
XX DT 08-NOV-1999 (first entry)
XX DE Human Apo B protein fragment.
XX KW Apo E; Apo B; hyperlipidemia; human; treatment; hepatocyte; apoprotein;
XX KW Apo A1; low density lipoprotein; LDL; blood; therapy; atherosclerosis;
XX KW high density lipoprotein; HDL; cholesterol; coronary heart disease;
XX KW Alzheimer's disease; hypobetalipoproteinemia; dysbetalipoproteinemia.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT 1..3923
FT Protein /label= Apo B
FT /note= "Partial sequence, no start codon given"
XX PN WO9940789-A1.
XX 19-AUG-1999.
XX 28-AUG-1998; 98WO-US017908.
XX 12-FEB-1998; 98US-0074497P.
XX 30-JUN-1998; 98US-00108006.
XX PA (MINU) UNIV MINNESOTA.
XX PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
XX PI Steer CJ, Kren BT, Bandyopadhyay PT, Roy-Chowdhury J;
XX WPI, 1999-527333/44.
XX N-PSDB; AA209525.
XX PT Mutating apolipoprotein genes in hepatocytes to control cholesterol
XX PT levels, e.g. for treating or preventing hyperlipidemia, particularly
XX PT atherosclerosis.
XX PS Claim 4; Page 75-83; 106pp; English.
XX This invention describes a novel method for the genetic treatment of
XX hyperlipidemia by altering genes, in hepatocytes, for apoprotein (apo) B,
XX E or A1. Low density lipoprotein (LDL) levels in the blood are reduced by
XX altering an apo B gene (II) in a hepatocyte. The invention describes a
XX method for the therapeutic and/or prophylactic method involving altering
XX an apo E gene in hepatocytes by introducing the mutations Arg12Cys,
XX Arg158Gly or Cys158Arg and a method for ameliorating atherosclerosis by
XX altering the apo A1 gene in a hepatocyte so that the altered protein can
XX dimerize. Altering expression of apo genes regulates levels of high and
XX low density lipoprotein cholesterol. Altering expression of apo B, E and
XX A1 genes is used to treat or prevent atherosclerosis, coronary heart
XX disease, Alzheimer's disease, hypobetalipoproteinemia, and
XX dysbetalipoproteinemia. This sequence represents a fragment of the human
XX Apo B protein described in the method of the invention
SQ Sequence 3923 AA;

Query Match 95.2%; Score 60; DB 2; Length 3923;
Best Local Similarity 90.9%; Pred. No. 0.26;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAEYKKNKRRH 11
DB 2534 KAQYKKNKRRH 2544
RESULT 10
AAM41262
ID AAM41262 standard; peptide, 4536 AA.
XX AAM41262;
XX AC
XX DT 19-MAY-1998 (first entry)
XX DE Apolipoprotein B-100.
XX KW Anti-coagulant; apolipoprotein B-100; apob-100; metastatic spread;
XX KW thromboplastin-mediated process; cancer; inhibitor; blood coagulation;
XX KW angiogenesis; cellular differentiation; apoptosis; KRAD-14;
XX KW prothrombinase complex.
XX OS Homo sapiens.
XX PN WO9743311-A1.
XX 20-NOV-1997.
XX 09-MAY-1997; 97WO-GB001255.
XX 09-MAY-1996; 96GB-00009702.
XX (UNLO) ROYAL FREE HOSPITAL SCHOOL MED.
XX Bruckdorfer KR, Etelate C;
XX WPI, 1998-008798/01.
XX DR
XX PT Peptide fragments of apo:liipo:protein B-100 with anticoagulant activity -
XX PT used for treating or preventing coagulation, inhibiting angiogenesis,
XX PT cell differentiation and apoptosis.
XX PS Disclosure; Page 42-47; 60pp; English.
XX This sequence represents the human apolipoprotein B-100 (apob-100).
XX Fragments of this sequence can be used in the peptide of the invention,
XX which has the formula (I), or their variants with one or more internal
XX deletions, insertions or substitutions, while retaining anti-coagulant
XX properties of apolipoprotein B-100 (apob-100). Z1-KAQ-X1-KKNKRRHS-X2-T-Z2
XX (I); X1 = S or Y; X2 = T or I; Z1 = the N terminus of the peptide, or 1-
XX 47 amino acids (aa); Z2 = the C terminus of the peptide, a terminal amide
XX group or 1-77 aa. Compositions containing the peptide are used for
XX simultaneous, separate or sequential treatment of cancer, particularly to
XX prevent metastatic spread. They are also used to inhibit thromboplastin-
XX mediated processes, specifically to prevent or reduce blood coagulation
XX (e.g. during or after surgery or in cases of heart attack, stroke etc.)
XX and to inhibit angiogenesis, cellular differentiation or apoptosis. KRAD-
XX 14, which is active as such or as part of a 98-aa peptide, inhibits
XX activation of the prothrombinase complex; and prevents activation of
XX factor VII on the surface of thromboplastin and of platelets by thrombin.
XX It binds to the residues 58-66 of thromboplastin. Since (I) are much
XX smaller than apob-100, they act more quickly
SQ Sequence 4536 AA;
Query Match 95.2%; Score 60; DB 2; Length 4536;
Best Local Similarity 90.9%; Pred. No. 0.31;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAEYKKNKRRH 11

Db 3147 KAQYKKNKRRH 3157

RESULT 11

AAW96826
ID AAW96826 standard; protein; 4536 AA.

XX KAQYKKNKRRH 3157

AC AAW96826;

XX 22-APR-1999 (first entry)

DE Amino acid sequence of human apolipoprotein B-100 (apoB-100).

XX Homo sapiens.

XX WO9856938-A1.

XX 17-DEC-1998.

XX 10-JUN-1998; 98WO-US011927.

XX 13-JUN-1997; 97US-00874807.

XX 14-MAY-1998; 98US-00079030.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX Guevara JG, Hoogveen RC, Moore JP;

XX WPI; 1999-070331/06.

XX Composition comprising nucleic acid bound to LDL or VLDL lipoprotein -

XX treatment.

XX Disclosure; Fig 1A-C; 293pp; English.

XX The present sequence represents human apolipoprotein B-100 (apoB-100).

XX ApoB-100 is a major apolipoprotein component of very-low density lipoproteins

XX ((LDL)), intermediate density lipoprotein (IDL), low density lipoproteins

XX comprises LDL and apolipoproteins for the binding and in vivo transport

XX of nucleic acids. Binding domains (see AAW96827-77) and nuclear

XX localization sequences (see AAW96878-97) for use in the composition can

XX be derived from the present sequence. The composition is used to deliver

XX therapeutic polypeptide or antisense molecule (or ribozyme). Specifically

XX they are used for gene therapy of cancers (particularly non-small cell

XX lung carcinoma), diabetes, cystic fibrosis and arteriosclerosis

SO Sequence 4536 AA;

Query Match

Best Local Similarity 95.2%; Score 60; DB 2; Length 4536;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAQYKKNKRRH 11

DB 3147 KAQYKKNKRRH 3157

RESULT 12

AAU98981

XX AAU98981 standard; protein; 4560 AA.

AC AAU98981;

XX 05-NOV-2002 (first entry)

XX DE Human apolipoprotein B100 (apoB100).

XX Human; low density lipoprotein receptor; LDLR; apolipoprotein E; apoE;

XX virus-lipoprotein complex; apolipoprotein B100; apoB100; VSV;

XX Flaviviridae virus; vesicular stomatitis virus; cholesterol metabolism.

XX Homo sapiens.

XX Key

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

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XX Region

XX Region

Claim 11, Page 44-47; 49pp; English.

The invention relates to a method of inhibiting infection of a cell by

lipoprotein, by preventing formation of and altering conformation of complex,

or blocking cell receptor for the complex using antibody to receptor.

The invention relates to a method of inhibiting infection of a cell by

lipoprotein, by preventing formation of and altering conformation of complex,

or blocking cell receptor for the complex using antibody to receptor.

The invention relates to a method of inhibiting infection of a cell by

lipoprotein, by preventing formation of and altering conformation of complex,

or blocking cell receptor for the complex using antibody to receptor.

The invention relates to a method of inhibiting infection of a cell by

lipoprotein, by preventing formation of and altering conformation of complex,

or blocking cell receptor for the complex using antibody to receptor.

The invention relates to a method of inhibiting infection of a cell by

lipoprotein, by preventing formation of and altering conformation of complex,

or blocking cell receptor for the complex using antibody to receptor.

RESULT 13

Db 3171 KAQYKKNKRRH 3181

Query Match

Best Local Similarity 95.2%; Score 60; DB 5; Length 4560;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAQYKKNKRRH 11

DB 3171 KAQYKKNKRRH 3181

ADD48677
 ID ADD48677 standard; protein; 4561 AA.
 XX
 AC ADD48677;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein X04714, SEQ ID NO 14384.
 XX
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX
 OS Homo sapiens.
 XX
 PN WO2003016475-A2.
 PD
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002MO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'Urso D, Befort K, Costigan M;
 XX
 DR WPI; 2003-268312/26.
 DR GENBANK; X04714.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 SO Sequence 4561 AA;

Query Match 95.2%; Score 60; DB 7; Length 4561;
 Best Local Similarity 90.9%; Pred. No. 0.31;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KAEYKKNKGRH 11

Db 3171 KAEYKKNKGRH 3181
 ||:|||||
 RESULT 14
 ID AAO15893
 ID AAO15893 standard; protein; 4563 AA.
 XX
 AC AAO15893;
 XX
 DT 30-JAN-2003 (first entry)
 XX
 DE Human apolipoprotein B (APOB).
 XX
 KW Human; gene therapy; single nucleotide polymorphism; SNP;
 KW cytochrome C oxidase subunit VIb; COX6B; high serum cholesterol; GPI-1;
 KW N-acetylglucosaminyl transferase component; cardiovascular disease; HDL;
 KW glycosylphosphatidylinositol-1; low serum high density lipoprotein.
 XX
 OS Homo sapiens.
 XX
 PN WO200272604-A2.
 PD
 PD 19-SEP-2002.
 XX
 PF 05-MAR-2002; 2002MO-US006728.
 XX
 PR 09-MAR-2001; 2001US-00802640.
 XX
 PA (SEQU-) SEQUENOM INC.
 XX
 PI Braun A, Banaal A, Klaym PW;
 XX
 DR WPI; 2002-750478/81.
 DR N-PSDB; ABT13015.
 XX
 PT Detecting the presence or absence of an allelic variant of a polymorphic
 PT region of COX6B and/or GPI-1 gene, useful for detecting a predisposition
 PT to high serum cholesterol, low serum HDL and cardiovascular disease.
 XX
 PS Disclosure; Page 158-168; 199pp; English.
 XX
 CC The invention comprises methods of detecting the presence or absence of
 CC at least one allelic variant of a polymorphic region of a gene associated
 CC with cardiovascular disease. The invention specifically relates to
 CC detecting the region of a cytochrome C oxidase subunit VIb (COX6B) gene
 CC that is associated with high serum cholesterol, or the region of the N-
 CC acetylglucosaminyl transferase component glycosylphosphatidylinositol-1
 CC (GPI-1) gene that is associated with low serum high density lipoprotein
 CC (HDL). The methods of the invention are useful for detecting a
 CC predisposition to high serum cholesterol, low serum HDL and
 CC cardiovascular disease. The methods are also useful for elucidating
 CC pathological pathways, developing diagnostic assays and new drug
 CC therapies for such disorders. The present amino acid sequence represents
 CC a human protein that is associated with high serum cholesterol, low serum
 CC HDL and/or cardiovascular disease
 CC
 XX
 SO Sequence 4563 AA;

Query Match 95.2%; Score 60; DB 5; Length 4563;
 Best Local Similarity 90.9%; Pred. No. 0.31;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KAEYKKNKGRH 11

RESULT 15
 ID ABR40253
 ID ABR40253 standard; protein; 4563 AA.
 XX
 AC ABR40253;

Search completed: January 12, 2005, 13:25:39
Job time : 103.484 secs

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XX 20-JUN-2003 (first entry)
DT
XX
DE Human alipoprotein B.
XX
KW Human; alipoprotein B; Apob; antilipemic; antiarteriosclerotic;
KW antidiabetic; anorectic; cardiovascular; gene therapy; lipid metabolism;
KW cholesterol metabolism; atherosclerosis; hyperlipidaemia; diabetes;
KW type 2 diabetes; obesity; atherosclerosis; cardiovascular disease;
KW glucose.
XX
OS Homo sapiens.
XX
PN WO2003011887-A2.
XX
PD 13-FEB-2003.
XX
PF 30-JUL-2002; 2002MO-US024247.
XX
PR 01-AUG-2001; 2001US-00920033.
PR 30-APR-2002; 2002US-00135985.
PR 15-MAY-2002; 2002US-00147196.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Crooke RM, Graham MJ;
XX
DR WPI; 2003-268105/26.
DR N-PSDB; ACC62114.
XX
PT New antisense oligonucleotides for modulating apolipoprotein B,
PT especially for preventing or treating atherosclerosis, hyperlipidemia or
PT diabetes, or for modulating glucose, cholesterol, lipoprotein or
PT triglyceride levels.
XX
PS Disclosure; Page 118-138; 160pp; English.
XX
CC The invention relates to a novel compound that is 8-50 nucleotides in
CC length that is targeted to a nucleic acid molecule encoding
CC apolipoprotein B (ApoB), and specifically hybridises with and inhibits
CC the expression of a nucleic acid molecule encoding ApoB; or which
CC specifically hybridises with at least an 8-nucleotide portion of an
CC active site on a nucleic acid molecule encoding ApoB. A compound of the
CC invention has antilipemic, antiarteriosclerotic, antidiabetic,
CC anorectic, and cardiovascular activity. The compound may have a use in
CC gene therapy. The antisense oligonucleotide is useful for treating an
CC animal having a disease or conditions associated with ApoB, e.g. a
CC condition involving abnormal lipid metabolism, atherosclerosis, diabetes
CC abnormal cholesterol metabolism, atherosclerosis, or a condition
CC involving an abnormal metabolic condition (e.g. hyperlipidaemia, diabetes
CC specifically Type 2 diabetes), obesity, atherosclerosis, diabetes
CC cardiovascular disease). The new compound or the antisense
CC oligonucleotide is also useful for modulating glucose levels
CC (particularly plasma or serum glucose levels) in a human or diabetic
CC animal, or for modulating serum cholesterol levels, lipoprotein levels
CC (specifically VLDL, HDL or LDL) or serum triglyceride levels,
CC particularly in a human. The antisense compound is also useful for
CC preventing or delaying the onset of a disease or condition associated
CC with ApoB, or the onset of an increase in glucose levels in the animal or
CC human. The present sequence is used in the exemplification of the
CC invention
XX
SQ Sequence 4563 AA;

```

Query Match 95.2%; Score 60; DB 6; Length 4563;
Best Local Similarity 90.9%; Pred. No. 0.31;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
||:|||||||
||:|||||||
Db 3174 KAEYKKNKRRH 3184

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OM protein - protein search, using sw model

Run on: January 12, 2005, 13:14:21 ; Search time 25.9032 Seconds
(without alignments)
28.162 Million cell updates/sec

Title: US-10-657-404A-1
Perfect score: 63
Sequence: 1 KAEYKKNKRRH 11

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
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- 5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63	100.0	11	US-09-269-533A-1	Sequence 1, Appli
2	60	95.2	14	US-09-180-422B-19	Sequence 19, Appli
3	60	95.2	50	US-09-079-030-97	Sequence 97, Appli
4	60	95.2	138	US-09-180-422B-12	Sequence 12, Appli
5	60	95.2	394	US-09-079-030-83	Sequence 83, Appli
6	60	95.2	840	US-09-079-030-214	Sequence 214, Appli
7	60	95.2	4536	US-09-180-422B-27	Sequence 27, Appli
8	60	95.2	4536	US-09-079-030-1	Sequence 1, Appli
9	60	95.2	4563	US-09-108-006C-1	Sequence 1, Appli
10	60	95.2	4563	US-09-538-092-842	Sequence 842, Appli
11	60	95.2	12	US-09-180-422B-9	Sequence 9, Appli
12	52	82.5	13	US-09-180-422B-11	Sequence 11, Appli
13	52	82.5	14	US-09-180-422B-1	Sequence 1, Appli
14	52	82.5	18	US-09-079-030-204	Sequence 204, Appli
15	51	81.0	14	US-09-180-422B-18	Sequence 18, Appli
16	48	76.2	773	US-09-079-030-215	Sequence 215, Appli
17	47	74.6	10	US-09-180-422B-6	Sequence 6, Appli
18	47	74.6	11	US-09-180-422B-8	Sequence 8, Appli
19	47	74.6	12	US-09-180-422B-10	Sequence 10, Appli
20	47	74.6	43	US-09-079-030-164	Sequence 164, Appli
21	43	68.3	9	US-09-180-422B-5	Sequence 5, Appli
22	43	68.3	10	US-09-180-422B-7	Sequence 7, Appli
23	43	68.3	785	US-09-079-030-216	Sequence 216, Appli
24	42	66.7	269	US-09-270-767-37552	Sequence 37552, A
25	42	66.7	269	US-09-270-767-37552	Sequence 37552, A
26	41	65.1	1213	US-08-188-582-20	Sequence 20, Appli
27	41	65.1	1213	US-08-646-715-20	Sequence 20, Appli

ALIGNMENTS

28	39	61.9	9	4	US-09-180-422B-4	Sequence 4, Appli
29	38	60.3	215	3	US-09-134-001C-3249	Sequence 3249, Ap
30	38	60.3	308	4	US-09-248-796A-19781	Sequence 19781, A
31	38	60.3	345	4	US-09-198-452A-89	Sequence 89, Appli
32	38	60.3	491	4	US-09-248-796A-19540	Sequence 19540, A
33	37	58.7	141	4	US-09-328-352-7100	Sequence 7100, Ap
34	37	58.7	156	4	US-09-889-463A-8	Sequence 8, Appli
35	37	58.7	207	4	US-09-270-767-61968	Sequence 61968, A
36	37	58.7	208	4	US-09-270-767-60040	Sequence 60040, A
37	37	58.7	340	4	US-09-270-767-43111	Sequence 43111, A
38	37	58.7	410	4	US-09-270-767-44592	Sequence 44592, A
39	37	58.7	598	4	US-09-538-092-1083	Sequence 1083, Ap
40	37	58.7	601	4	US-09-252-991A-23280	Sequence 23280, A
41	37	58.7	601	4	US-09-889-463A-10	Sequence 10, Appli
42	37	58.7	913	1	US-08-220-151-6	Sequence 6, Appli
43	37	58.7	913	1	US-08-413-118-6	Sequence 6, Appli
44	37	58.7	913	3	US-08-473-446-6	Sequence 6, Appli
45	37	58.7	913	3	US-09-232-468A-2	Sequence 2, Appli

APPL:CONF

RESULT 1
US-09-269-533A-1
Sequence 1, Application US/09269533A
Patent No. 6670452
GENERAL INFORMATION:
APPLICANT: University of Strathclyde
APPLICANT: Halbert, Gavin
APPLICANT: Owens, Moira
APPLICANT: Bailly, George
TITLE OF INVENTION: No. 6670452-Naturally Occurring Lipoprotein Particle
FILE REFERENCE: P07885US
CURRENT APPLICATION NUMBER: US/09/269, 533A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: PCT/GB97/02610
PRIOR FILING DATE: 1997-09-25
PRIOR APPLICATION NUMBER: GB 9620153.8
PRIOR FILING DATE: 1996-09-27
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc feature
LOCATION: ()
OTHER INFORMATION: Apo B binding site sequence
US-09-269-533A-1
Query Match 100.0%; Score 63; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 KAEYKKNKRRH 11
DB 1 KAEYKKNKRRH 11
RESULT 2
US-09-180-422B-19
Sequence 19, Application US/09180422B
Patent No. 6444644
GENERAL INFORMATION:
APPLICANT: BRUCKDORFER, KARL R
APPLICANT: ETTREICH, CAMILLE
TITLE OF INVENTION: ANTICOAGULANT PEPTIDE FRAGMENTS DERIVED FROM APOLIPOPROTEIN B-100
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NIXON & VANDERHAYE, P.C.

us-10-657-404a-1.ra1

STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/180,422B
FILING DATE: 07-Dec-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36663
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164100
TELEFAX: 7038164000
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
Query Match
Best Local Similarity 95.2%; Score 60; DB 4; Length 14;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KAEYKKNKRRH 11
Db 1 KAEYKKNKRRH 11

RESULT 3
US-09-079-030-97
Sequence 97, Application US/09079030
Patent No. 6635623
GENERAL INFORMATION:
APPLICANT: Guevera, Jr., Juan G.
APPLICANT: Hoogveen, Ron C.
TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
TITLE OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
NUMBER OF SEQUENCES: 229
CORRESPONDENCE ADDRESS:
ADDRESS: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,030
FILING DATE: 07-Dec-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMillian, Nabeela R.
REGISTRATION NUMBER: P-43,363
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-079-030-97
Query Match
Best Local Similarity 95.2%; Score 60; DB 4; Length 50;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KAEYKKNKRRH 11
Db 2 KAEYKKNKRRH 12

RESULT 4
US-09-180-422B-12
Sequence 12, Application US/09180422B
Patent No. 644664
GENERAL INFORMATION:
APPLICANT: BRUCKDORFER, KARL R
TITLE OF INVENTION: ANTICOMULANT PEPTIDE FRAGMENTS DERIVED
FROM APOLIPROTEIN B-100
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESS: NIXON & VANDERHOF, P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/180,422B
FILING DATE: 07-Dec-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36663
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164100
TELEFAX: 7038164000
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-180-422B-12
Query Match
Best Local Similarity 95.2%; Score 60; DB 4; Length 138;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KAEYKKNKRRH 11
Db 48 KAEYKKNKRRH 58

RESULT 5
US-09-079-030-83
Sequence 83, Application US/09079030

Patent No. 6635623
GENERAL INFORMATION:
APPLICANT: Guevera, Jr., Juan G.
APPLICANT: Hoogveen, Ron C.
TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
NUMBER OF SEQUENCES: 229
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,030
FILING DATE: Concurrently Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMillian, Nabeha R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: ARAG:003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-079-030-83

Query Match 95.2% Score 60; DB 4; Length 394;
Best Local Similarity 90.9%; Pred. No. 0.013;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAEYKKNGRH 11
||:|||||||
Db 218 KAQYKKNGRH 228

RESULT 6
US-09-079-030-214
Sequence 214, Application US/09079030
Patent No. 6635623
GENERAL INFORMATION:
APPLICANT: Guevera, Jr., Juan G.
APPLICANT: Hoogveen, Ron C.
TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
NUMBER OF SEQUENCES: 229
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,030

FILING DATE: Concurrently Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMillian, Nabeha R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: ARAG:003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-079-030-214

Query Match 95.2% Score 60; DB 4; Length 840;
Best Local Similarity 90.9%; Pred. No. 0.028;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAEYKKNGRH 11
||:|||||||
Db 447 KAQYKKNGRH 457

RESULT 7
US-09-180-422B-27
Sequence 27, Application US/09180422B
Patent No. 6444644
GENERAL INFORMATION:
APPLICANT: BRUCKDORFER, KARL R
ETTELDE, CAMILLE
TITLE OF INVENTION: ANTICOAGULANT PEPTIDE FRAGMENTS DERIVED
FROM APOLIPOPROTEIN B-100
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE, P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/180,422B
FILING DATE: 07-Dec-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36663
REFERENCE/DOCKET NUMBER: 117-268
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164100
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 4536 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-180-422B-27

Query Match 95.2% Score 60; DB 4; Length 4536;
Best Local Similarity 90.9%; Pred. No. 0.15;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Thu Jan 13 09:04:54 2005

US-10-657-404a-1.ral

OY 1 KAEYKONKRRH 11
DB 3147 KAEYKONKRRH 3157

RESULT 8

US-09-079-030-1
Sequence 1, Application US/09079030
Patent No. 663623
GENERAL INFORMATION:
APPLICANT: Guevera, Jr., Juan G.
APPLICANT: Hoocheven, Ron C.
TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
NUMBER OF INVENTION: VECTORS FOR TRANSCRIPTION OF EUKARYOTIC CELLS
CORRESPONDENCE ADDRESSES: 229
ADDRESS: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent, PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 60/074, 497
FILING DATE: 30-APR-1998
ATTORNEY/AGENT INFORMATION:
NAME: McMillan, Nabeela R.
REGISTRATION NUMBER: P-43,363
TELECOMMUNICATION INFORMATION: ARAG:003
TELEPHONE: 512/418-3000
TELEFAX: 512/418-3000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4536 amino acids
TYPE: amino acid
STRANDEDNESS: linear
US-09-079-030-1

Query Match
Best Local Similarity 95.2%; Score 60; DB 4; Length 4536;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 KAEYKONKRRH 11
DB 3147 KAEYKONKRRH 3157

RESULT 9

US-09-108-006C-1
Sequence 1, Application US/09108006C
Patent No. 6524613
GENERAL INFORMATION:
APPLICANT: Steer, Clifford J.
Klen, Betsy T.
Bandyopadhyay, Parmita
Roy-Chowdhury, Jayanta
NUMBER OF INVENTION: Hepatocellular Chimeraplasty
CORRESPONDENCE ADDRESSES: 62
ADDRESS: Kimeragen, Inc.
STREET: 300 Pleasant Run
CITY: Newtown
STATE: PA
COUNTRY: USA

ZIP: 18940
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: Paateseq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/108,006C
FILING DATE: 30-Jun-1992
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,288
FILING DATE: 30-APR-1997
APPLICATION NUMBER: 60/054,837
FILING DATE: 05-AUG-1997
APPLICATION NUMBER: 60/064,996
FILING DATE: 10-NOV-1997
APPLICATION NUMBER: 60/074,497
FILING DATE: 12-FEB-1998
APPLICATION NUMBER: PCT US 98/08834
FILING DATE: 30-APR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Friedel, Thomas
REGISTRATION NUMBER: 29258
TELECOMMUNICATION INFORMATION: 7991-015-999
TELEPHONE: 215-504-4444
TELEFAX: 215-504-4545
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4563 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
US-09-108-006C-1

Query Match
Best Local Similarity 95.2%; Score 60; DB 4; Length 4563;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 KAEYKONKRRH 11
DB 3174 KAEYKONKRRH 3184

RESULT 10

US-09-538-092-842
Sequence 842, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Glot, Iolc
TITLE OF INVENTION: Protein A.
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 178,965
SOFTWARE: CurataseqFormat Version 0.9
SEQ ID NO 842
LENGTH: 4563
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)..(0)
OTHER INFORMATION: Polypeptide Accession Number P04114

US-09-538-092-842

Query Match 95.2%; Score 60; DB 4; Length 4563;
Best Local Similarity 90.9%; Pred. No. 0.15;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
||:|||||
Db 3174 KAOXKKNKRRH 3184

RESULT 11

US-09-180-422B-9
; Sequence 9, Application US/09180422B
; Patent No. 6444644
; GENERAL INFORMATION:
; APPLICANT: BRUCKDORFER, KARL R
; ETTLELAIE, CAMILLE
; TITLE OF INVENTION: ANTICOAGULANT PEPTIDE FRAGMENTS DERIVED
; FROM APOLIPOPROTEIN B-100
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE, P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Releasee #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/180,422B
; FILING DATE: 07-Dec-1998
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36663
; REFERENCE/DOCKET NUMBER: 117-268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164000
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "Xaa can be Ser or Tyr"
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-180-422B-9

Query Match 82.5%; Score 52; DB 4; Length 12;
Best Local Similarity 81.8%; Pred. No. 0.01;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
||:|||||
Db 1 KAOXKKNKRRH 11

RESULT 12
US-09-180-422B-11
; Sequence 11, Application US/09180422B
; Patent No. 6444644
; GENERAL INFORMATION:
; APPLICANT: BRUCKDORFER, KARL R

ETTLELAIE, CAMILLE

TITLE OF INVENTION: ANTICOAGULANT PEPTIDE FRAGMENTS DERIVED
FROM APOLIPOPROTEIN B-100

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE, P.C.

STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Releasee #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/180,422B

FILING DATE: 07-Dec-1998

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: SADOFF, B.J.

REGISTRATION NUMBER: 36663

REFERENCE/DOCKET NUMBER: 117-268

TELECOMMUNICATION INFORMATION:

TELEPHONE: 7038164000

TELEFAX: 7038164100

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Modified-site

LOCATION: 4

OTHER INFORMATION: /note= "Xaa can be Ser or Tyr"

FEATURE:

NAME/KEY: Modified-site

LOCATION: 13

OTHER INFORMATION: /note= "Xaa can be Thr or Ile"

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-180-422B-11

Query Match 82.5%; Score 52; DB 4; Length 13;
Best Local Similarity 81.8%; Pred. No. 0.011;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
||:|||||
Db 1 KAOXKKNKRRH 11

RESULT 13

US-09-180-422B-1
; Sequence 1, Application US/09180422B
; Patent No. 6444644
; GENERAL INFORMATION:
; APPLICANT: BRUCKDORFER, KARL R
; ETTLELAIE, CAMILLE
; TITLE OF INVENTION: ANTICOAGULANT PEPTIDE FRAGMENTS DERIVED
; FROM APOLIPOPROTEIN B-100
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE, P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk

us-10-657-404a-1.rai

Page 6

0.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2005, 13:31:02 ; Search time 88.3548 Seconds
(without alignments)
44,980 Million cell updates/sec

Title: US-10-657-404A-1
Perfect score: 63
Sequence: 1 KAEYKKNKRRH 11

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Gapop 10.0, Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/FCI_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10D_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	63	100.0	11	9	US-09-269-533A-1
2	63	100.0	11	17	US-10-657-404A-1
3	60	95.2	20	15	US-10-333-313-2
4	60	95.2	24	15	US-10-333-313-5
5	60	95.2	3000	16	US-10-741-601-431
6	60	95.2	4563	9	US-09-870-759-128
7	60	95.2	4563	10	US-09-802-640-32
8	60	95.2	4563	10	US-09-751-708A-128
9	60	95.2	4563	14	US-10-403-902A-32
10	60	95.2	4563	16	US-10-741-601-432
11	60	95.2	4563	16	US-10-741-601-433
12	60	95.2	4563	17	US-10-428-817A-124
13	47	74.6	20	14	US-10-115-072-14

14	47	74.6	20	17	US-10-679-032-52	Sequence 52, App1
15	44	69.8	68	17	US-10-425-115-343636	Sequence 343636, App1
16	44	69.8	73	17	US-10-425-115-324738	Sequence 324738, App1
17	44	69.8	160	15	US-10-424-599-249584	Sequence 249584, App1
18	44	69.8	201	15	US-10-425-114-70425	Sequence 70425, A
19	44	69.8	205	17	US-10-425-115-357812	Sequence 357812, A
20	44	69.8	216	15	US-10-425-114-68080	Sequence 68080, A
21	44	69.8	218	17	US-10-425-115-313121	Sequence 313121, A
22	44	69.8	899	16	US-10-437-963-122313	Sequence 122313, A
23	41	65.1	217	17	US-10-425-115-218015	Sequence 218015, A
24	41	65.1	218	15	US-10-425-115-64096	Sequence 64096, A
25	41	65.1	266	16	US-10-437-963-203619	Sequence 203619, A
26	40	63.5	75	15	US-10-424-599-266670	Sequence 266670, App1
27	40	63.5	100	17	US-10-425-115-200681	Sequence 200681, App1
28	40	63.5	769	15	US-10-342-844-90	Sequence 90, App1
29	39	61.9	10	10	US-09-572-404B-845	Sequence 845, App1
30	39	61.9	54	17	US-10-425-115-198721	Sequence 198721, App1
31	39	61.9	79	17	US-10-425-115-326337	Sequence 326337, App1
32	39	61.9	488	16	US-10-437-963-178827	Sequence 178827, App1
33	38	60.3	125	17	US-10-425-115-218016	Sequence 218016, App1
34	38	60.3	345	15	US-10-289-762-89	Sequence 89, App1
35	38	60.3	487	15	US-10-282-122A-51517	Sequence 51517, A
36	37	58.7	68	10	US-09-764-891-4346	Sequence 4346, App1
37	37	58.7	68	14	US-10-205-428-375	Sequence 375, App1
38	37	58.7	79	15	US-10-424-599-245751	Sequence 245751, App1
39	37	58.7	84	14	US-10-023-896-61	Sequence 61, App1
40	37	58.7	84	14	US-10-023-896-88	Sequence 88, App1
41	37	58.7	86	15	US-10-424-599-234991	Sequence 234991, App1
42	37	58.7	88	17	US-10-425-115-360031	Sequence 360031, App1
43	37	58.7	89	14	US-10-029-386-29235	Sequence 29235, A
44	37	58.7	97	9	US-09-925-300-944	Sequence 944, App1
45	37	58.7	127	17	US-10-425-115-191644	Sequence 191644, App1

ALIGNMENTS

Application

RESULT 1
US-09-269-533A-1 ; Sequence 1, Application US/09269533A
; Patent No. US20020147304A1
; GENERAL INFORMATION:
; APPLICANT: University of Strathclyde
; APPLICANT: Halbert, Gavin
; APPLICANT: Owens, Moira
; TITLE OF INVENTION: No. US20020147304A1-Naturally Occurring Lipoprotein Particle
; FILE REFERENCE: P078985US
; CURRENT APPLICATION NUMBER: US/09/269, 533A
; CURRENT FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: PCT/GB97/02610
; PRIOR FILING DATE: 1997-09-25
; PRIOR APPLICATION NUMBER: GB 9620153.8
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; TYPE: PRT
; LENGTH: 11
; ORGANISM: Artificial Sequence
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (1..11)
; OTHER INFORMATION: Apo B binding site sequence
US-09-269-533A-1
Query Match 100.0%; Score 63; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 KAEYKKNKRRH 11
Db 1 KAEYKKNKRRH 11

RESULT 2
US-10-657-404a-1
Sequence 1, Application US/10657404A
Publication No. US20040235730A1
GENERAL INFORMATION:
APPLICANT: University of Strathclyde
APPLICANT: Halbert, Gavin
APPLICANT: Owens, Molra
TITLE OF INVENTION: Non-naturally Occurring Lipoprotein Particle
FILE REFERENCE: P07885US-CIP
CURRENT APPLICATION NUMBER: US/10/657,404A
PRIOR FILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: PCT/GB97/02610
PRIOR FILING DATE: 1997-09-25
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Apo B binding site sequence
US-10-657-404a-1

Query Match
Best Local Similarity 100.0%; Score 63; DB 17; Length 11;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
DB 1 KAEYKKNKRRH 11

RESULT 3
US-10-333-313-2
Sequence 2, Application US/10333313
Publication No. US20040091934A1
GENERAL INFORMATION:
APPLICANT: Narvonen, Outi
TITLE OF INVENTION: Peptides and Their Use in Assays for Cardiovascular Disease
FILE REFERENCE: GJE-6363
CURRENT APPLICATION NUMBER: US/10/333,313
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: PCT/GB01/03212
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: oligopeptide
US-10-333-313-2

Query Match
Best Local Similarity 95.2%; Score 60; DB 15; Length 20;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
DB 4 KAEYKKNKRRH 14

RESULT 4
US-10-333-313-5

Sequence 5, Application US/10333313
Publication No. US20040091934A1
GENERAL INFORMATION:
APPLICANT: Narvonen, Outi
TITLE OF INVENTION: Peptides and Their Use in Assays for Cardiovascular Disease
FILE REFERENCE: GJE-6363
CURRENT APPLICATION NUMBER: US/10/333,313
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: PCT/GB01/03212
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 24
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: oligopeptide
US-10-333-313-5

Query Match
Best Local Similarity 95.2%; Score 60; DB 15; Length 24;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
DB 6 KAEYKKNKRRH 16

RESULT 5
US-10-741-601-431
Sequence 431, Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: CI.001508
CURRENT APPLICATION NUMBER: US/10/741,601
PRIOR FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 431
LENGTH: 3000
TYPE: PRT
ORGANISM: Homo sapiens
US-10-741-601-431

Query Match
Best Local Similarity 95.2%; Score 60; DB 16; Length 3000;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
DB 2126 KAEYKKNKRRH 2136

RESULT 6
US-09-870-759-128
Sequence 128, Application US/09870759
Patent No. US20020177551A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
PRIOR FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
SEQ ID NO 128

LENGTH: 4563
TYPE: PRT
ORGANISM: Homo sapiens
US-09-870-759-128

Query Match
Best Local Similarity 95.2%; Score 60; DB 9; Length 4563;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAEYKKNKRRH 11
Db 3174 KAOYKKNKRRH 3184

RESULT 7

US-09-802-640-32
Sequence 32, Application US/09802640
Publication No. US20030036057A1

GENERAL INFORMATION:
APPLICANT: Braun, Andreas
APPLICANT: Kleya Patrick
TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: 24736-2048
CURRENT APPLICATION NUMBER: US/09/802,640
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 32
LENGTH: 4563
TYPE: PRT
ORGANISM: Homo sapien
US-09-802-640-32

Query Match
Best Local Similarity 95.2%; Score 60; DB 10; Length 4563;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAEYKKNKRRH 11
Db 3174 KAOYKKNKRRH 3184

RESULT 8

US-09-751-708A-128
Sequence 128, Application US/09751708A
Publication No. US20030157113A1

GENERAL INFORMATION:
APPLICANT: Terman, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 751708
CURRENT APPLICATION NUMBER: US/09/751,708A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 60/173,371
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
SEQ ID NO 128
LENGTH: 4563
TYPE: PRT
ORGANISM: Homo sapiens
US-09-751-708A-128

Query Match
Best Local Similarity 95.2%; Score 60; DB 10; Length 4563;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAEYKKNKRRH 11
Db 3174 KAOYKKNKRRH 3184

RESULT 9

US-10-403-902A-32
Sequence 32, Application US/10403902A
Publication No. US20030224418A1

GENERAL INFORMATION:
APPLICANT: Braun, Andreas
APPLICANT: Kleya, Patrick
TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: 24736-2048B
CURRENT APPLICATION NUMBER: US/10/403,902A
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: 09/802,640
PRIOR FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 32
LENGTH: 4563
TYPE: PRT
ORGANISM: Homo sapien
US-10-403-902A-32

Query Match
Best Local Similarity 95.2%; Score 60; DB 14; Length 4563;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAEYKKNKRRH 11
Db 3174 KAOYKKNKRRH 3184

RESULT 10

US-10-741-601-432
Sequence 432, Application US/10741601
Publication No. US20040166519A1

GENERAL INFORMATION:
APPLICANT: Cargill, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: CLO01500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 432
LENGTH: 4563
TYPE: PRT
ORGANISM: Homo sapiens
US-10-741-601-432

Query Match
Best Local Similarity 95.2%; Score 60; DB 16; Length 4563;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAEYKKNKRRH 11
Db 3174 KAOYKKNKRRH 3184

RESULT 11

US-10-741-601-433
Sequence 433, Application US/10741601
Publication No. US20040166519A1

GENERAL INFORMATION:
APPLICANT: Cargill, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: CLO01500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 433
LENGTH: 4563
TYPE: PRT
ORGANISM: Homo sapiens
US-10-741-601-433

Query Match
Best Local Similarity 95.2%; Score 60; DB 16; Length 4563;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAEYKKNKH 11
DB 3174 KAEYKKNKH 3184

RESULT 12
US-10-428-817A-124
Sequence 124, Application US/10428817A
Publication No. US20040214783A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
CURRENT APPLICATION NUMBER: US/10/428,817A
PRIOR FILING DATE: 2003-05-05
PRIOR APPLICATION NUMBER: US 60/378,988
PRIOR FILING DATE: 2002-05-08
PRIOR APPLICATION NUMBER: US 60/389,366
PRIOR FILING DATE: 2002-06-15
PRIOR APPLICATION NUMBER: US 60/406,697
PRIOR FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: US 60/406,750
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/415,310
PRIOR FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: US 60/415,400
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: US 60/438,686
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn version 3.2
SEQ ID NO 124
LENGTH: 4563
TYPE: PRT
ORGANISM: Homo sapiens
US-10-428-817A-124

Query Match
Best Local Similarity 95.2%; Score 60; DB 17; Length 4563;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAEYKKNKH 11
DB 3174 KAEYKKNKH 3184

RESULT 13
US-10-115-072-14
Sequence 14, Application US/10115072
Publication No. US20030105003A1
GENERAL INFORMATION:
APPLICANT: NILSSON, JAN
TITLE OF INVENTION: PEPTIDE-BASED IMMUNIZATION THERAPY FOR TREATMENT OF
TITLE OF INVENTION: ATHEROSCLEROSIS AND DEVELOPMENT OF PEPTIDE-BASED ASSAY
FILE REFERENCE: 03940 0057
CURRENT APPLICATION NUMBER: US/10/115,072
PRIOR FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: 60/281,410
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: SE 0101232-7

PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: SE 0103754-8
PRIOR FILING DATE: 2001-09-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-115-072-14

Query Match
Best Local Similarity 74.6%; Score 47; DB 14; Length 20;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKKNKH 9
DB 12 KAEYKKNKH 20

RESULT 14
US-10-679-032-52
Sequence 52, Application US/10679032
Publication No. US20040202653A1
GENERAL INFORMATION:
APPLICANT: NILSSON, JAN
APPLICANT: CARLSSON, ROLAND
APPLICANT: BENGTSSON, JENNY
APPLICANT: STRANDBERG, JERF
TITLE OF INVENTION: PEPTIDE-BASED PASSIVE IMMUNIZATION THERAPY FOR
FILE REFERENCE: 7303CIP
CURRENT APPLICATION NUMBER: US/10/679,032
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 52
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-679-032-52

Query Match
Best Local Similarity 74.6%; Score 47; DB 17; Length 20;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKKNKH 9
DB 12 KAEYKKNKH 20

RESULT 15
US-10-425-115-343636
Sequence 343636, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: LA ROSA, Thomas J.
APPLICANT: KOVALIC, David K.
APPLICANT: ZHOU, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
PRIOR FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 343636

LENGTH: 68
 TYPE: PRT
 ORGANISM: Zea mays
 FEATURE:
 OTHER INFORMATION: Clone ID: MRR4577_76558C.1.pep
 US-10-425-115-343636

Query Match 69.8%; Score 44; DB 17; Length 68;
 Best Local Similarity 77.8%; Pred. No. 9.6;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 EYKKKGRH 11
 |:|:|:|
 Db 1 EHKKKGRH 9

Search completed: January 12, 2005, 13:52:49
 Job time : 89.3548 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2005, 13:13:31 ; Search time 20.2256 Seconds
(without alignments)
52.328 Million cell updates/sec

Title: US-10-657-404a-1
Perfect score: 63
Sequence: 1 KAEYKKNKRRH 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	95.2	4563	1 LPHUB	apolipoprotein B-1
2	54	85.7	596	2 S32802	apolipoprotein B -
3	48	76.2	269	2 C60950	apolipoprotein B-1
4	48	76.2	779	2 JH0102	apolipoprotein B -
5	48	76.2	1778	2 J70382	apolipoprotein B -
6	48	76.2	2629	2 I46569	apolipoprotein B -
7	45	71.4	274	2 B60950	apolipoprotein B-1
8	43	68.3	784	2 A60950	apolipoprotein B-1
9	41.5	65.9	221	2 B4675	apolipoprotein B-1
10	41	65.1	1213	2 A54063	hypothetical prote
11	39	61.9	102	2 S09828	TATA-binding prote
12	39	61.9	102	2 S09828	hypothetical prote
13	39	61.9	365	2 I20958	hypothetical prote
14	39	61.9	452	2 H88337	protein F15A4.1 (i
15	39	61.9	734	2 S44617	C50C3.11 protein -
16	38	60.3	321	2 A42507	F5L protein - vacc
17	38	60.3	335	2 D72123	CT324 hypothetical
18	38	60.3	335	2 H86499	conserved membrane
19	38	60.3	343	2 G81547	probable membrane
20	38	60.3	487	2 C97144	oligosaccharinase
21	37	58.7	193	2 A62705	protein F14D16.9 (
22	37	58.7	206	2 D86323	probable oligopept
23	37	58.7	578	2 C71510	hypothetical prote
24	37	58.7	594	2 F82895	hypothetical prote
25	37	58.7	598	2 B40713	cyclicin I - human
26	37	58.7	697	2 H71525	probable outer mem
27	37	58.7	913	1 VGBEP5	glycoprotein gII p
28	37	58.7	1257	2 T28937	hypothetical prote
29	36	57.1	192	2 T02893	hypothetical prote

30	36	57.1	208	2 D65041	hypothetical prote
31	36	57.1	275	2 B60950	apolipoprotein B-1
32	36	57.1	324	2 T24819	hypothetical prote
33	36	57.1	354	2 AD1038	hypothetical prote
34	36	57.1	370	2 T37282	probable cathepsin
35	36	57.1	416	2 D71936	hypothetical prote
36	36	57.1	416	2 G64647	hypothetical prote
37	36	57.1	565	2 T47423	hypothetical prote
38	36	57.1	611	2 E71318	probable RNA polym
39	36	57.1	800	2 T00034	SART-1 protein - h
40	36	57.1	1818	1 S73852	hypothetical prote
41	35	55.6	123	2 S61173	hypothetical prote
42	35	55.6	138	2 S06571	finger protein (cl
43	35	55.6	217	2 UC7997	nucleolar protein,
44	35	55.6	224	2 S77828	probable transcrip
45	35	55.6	227	2 B84667	hypothetical prote

ALIGNMENTS

RESULT 1
LPHUB
apolipoprotein B-100 precursor - human
N:Contains: apolipoprotein B-26; apolipoprotein B-48; apolipoprotein B-74
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C:Accession: A27850; A25679; A25263; A25267; A25266; A24320; A24684; A23817; A25774; A264452; I61909; I59510; I39474; I39469; I84624; I37179; P50058
R:Ludwig, E.H.; Blackhart, B.D.; Pierotti, V.R.; Catali, L.; Fortier, C.; Knott, T.; Sco
DNA 6, 363-372, 1987
A:Title: DNA sequence of the human apolipoprotein B gene.
A:Reference number: A27850; MUID:86003974; PMID:3652907
A:Accession: A27850
A:Molecule type: DNA
A:Residues: 1-617, 'A', 619-1929, 'F', 1931-3318, 'D', 3320-3426, 'T', 3428-3431, 'Q', 3433-3731, 'A'
A:Cross-references: UNIPROT:P04114; UNIPROT:P78482; UNIPROT:P78479; UNIPROT:Q9UMN0; UNIP
R:Cladaras, C.; Hadzopoulos-Cladaras, M.; Nolte, R.T.; Atkinson, D.; Zannis, V.I.
EMBO J. 5, 3495-3507, 1986
A:Title: The complete sequence and structural analysis of human apolipoprotein B-100: re
A:Reference number: A91058; MUID:87161758; PMID:3030729
A:Accession: A25679
A:Molecule type: mRNA
A:Residues: 1-11, 15-2539, 'S', 2541-3823, 'R', 3825-4563 <CLA>
A>Note: 1109-AAP was also found
R:Knott, T.J.; Wallis, S.C.; Powell, L.M.; Pease, R.J.; Lunsig, A.J.; Blackhart, B.; McCa
Nucleic Acids Res. 14, 7501-7503, 1986
A:Title: Complete cDNA and derived protein sequence of human apolipoprotein B-100.
A:Reference number: A93639; MUID:87016385; PMID:3763409
A:Accession: A25263
A:Molecule type: mRNA
A:Residues: 1-272, 'N', 274-617, 'A', 619-1217, 'E', 1219-2091, 'V', 2093-2364, 'T', 2366-2679, 'Q'
A:Cross-references: GB:X04506; NID:G34330; PIDN:CAA28191.1; PID:G34331
R:Law, S.W.; Grant, S.M.; Higuchi, K.; Hoshitani, A.; Lackner, K.; Lee, N.; Brewer Jr
Proc. Natl. Acad. Sci. U.S.A. 83, 8143-8146, 1986
A:Title: Human liver apolipoprotein B-100 cDNA: complete nucleic acid and derived amino
A:Reference number: A94134; MUID:87041416; PMID:3464946
A:Accession: A25267
A:Molecule type: mRNA
A:Residues: 1-617, 'A', 619-703, 'P', 705-792, 'R', 794-1270, 'S', 1272-1866, 'G', 1868-2036, 'N', 2
4189-4220, 'W', 4222-4563 <LAW>
A>Note: the codons given for residues 704, 793, 1271, 2037, 2933, 3286, 3782, 4188, and
J.Chen, S.H.; Yang, C.Y.; Chen, P.P.; Senter, D.; Tanimura, M.; Li, W.H.; Gotto Jr., A.M.
J. Biol. Chem. 261, 12918-12921, 1986
A:Title: The complete cDNA and amino acid sequence of human apolipoprotein B-100.
A:Reference number: A92556; MUID:87008488; PMID:3759943
A:Accession: A25266
A:Molecule type: mRNA
A:Residues: 1-97, 'T', 99-328, 'V', 330-644, 'I', 646-918, 'P', 920-3318, 'D', 3320-3426, 'T', 3428-
9-4132, 'G', 4134-4180, 'E', 4182-4563 <CHE>
A:Cross-references: GB:U02610; NID:G178803; PIDN:AAA35549.1; PID:G178804
A>Note: a total of 2366 residues were confirmed by direct sequencing of tryptic peptides
R:Procter, A.A.; Hardman, D.A.; Sato, K.Y.; Schilling, J.W.; Yamamaka, M.; Hott, Y.J.; H

Proc. Natl. Acad. Sci. U.S.A. 83, 5678-5682, 1986
 A/Title: Analysis of cDNA clones encoding the entire B-26 region of human apolipoprotein B
 A/Reference number: A24320; MUID:86287319; PMID:3461454
 A/Accession: A24320
 A/Molecule type: mRNA
 A/Residues: 1-97, 'I', '99-617', 'A', '619-941', 'YYINSLPKP', '951-1138', 'PTGRLPNCFNSNGLICSLMHSFDF
 A/Cross-references: GB:M14081; NID:9178795; PIDN:AAA51752.1; PID:9553189
 R/Note: S.W.; Lackner, K.J.; Hospattanakar, A.V.; Anchors, J.M.; Sakaguchi, A.Y.; Naylor, R.
 Proc. Natl. Acad. Sci. U.S.A. 82, 8340-8344, 1985
 A/Title: Human apolipoprotein B-100: cloning, analysis of liver mRNA, and assignment of
 A/Reference number: A24684; MUID:86094221; PMID:3001697
 A/Accession: A24684
 A/Molecule type: mRNA
 A/Residues: 485-617, 'A', '619-1044' <LA2>
 A/Cross-references: GB:M12480; NID:9178791; PIDN:AAA51751.1; PID:9178792
 R/Note: Pictor, A.A.; Hardman, D.A.; Schilling, J.W.; Miller, J.; Appleby, V.; Chen, G.C.; K
 Proc. Natl. Acad. Sci. U.S.A. 83, 1467-1471, 1986
 A/Title: Isolation of a cDNA clone encoding the amino-terminal region of human apolipop
 A/Reference number: A94088; MUID:86149325; PMID:3513177
 A/Accession: A23817
 A/Molecule type: mRNA
 A/Residues: 1-291 <PRO>
 A/Cross-references: GB:M12681; NID:9178797; PIDN:AAA51753.1; PID:9178798
 R/Note: S.S.; Motulsky, A.G.; Albers, J.J.
 Proc. Natl. Acad. Sci. U.S.A. 82, 4983-4986, 1985
 A/Title: A partial cDNA clone for human apolipoprotein B
 A/Reference number: A25774; MUID:95270450; PMID:3860836
 A/Accession: A25774
 A/Molecule type: mRNA
 A/Residues: 705-791, 'SSSMKAAHQCPHSGAD', 810-906 <DEB>
 A/Cross-references: GB:K03175; NID:9178821; PIDN:AAA51759.1; PID:9178822
 R/Note: Carlson, P.; Darnofsky, C.; Olofsson, S.O.; Bjurell, G.
 Gene 49, 29-51, 1986
 A/Title: Analysis of the human apolipoprotein B gene: complete structure of the B-74 reg
 A/Reference number: A91565; MUID:87191999; PMID:2883086
 A/Accession: A26533
 A/Molecule type: mRNA
 A/Residues: 1282-2721, 2742-3290, 'L', '3292-3336', 'N', '3338-3948', 'F', '3950-3963', 'Y', '3965-4180',
 A/Cross-references: GB:M15421; NID:9178817; PIDN:AAA51758.1; PID:918818
 R/Note: Hardman, D.A.; Procter, A.A.; Chen, G.C.; Schilling, J.W.; Sato, K.Y.; Lau, K.; Yamana
 Biochemistry 26, 5478-5486, 1987
 A/Title: Structural comparison of human apolipoproteins B-48 and B-100.
 A/Reference number: A29671; MUID:88050832; PMID:3676265
 A/Accession: A29671
 A/Molecule type: mRNA
 A/Residues: 1671-2323, 'PYW', '2327-2352', 'H', '2354-2398' <HAR>
 A/Cross-references: GB:M17367; NID:9178731; PIDN:AAA51741.1; PID:9178732
 R/Note: R. Shoulters, C.C.; Myant, N.B.; Sicoli, A.; Rodriguez, J.C.; Cortese, C.; Baralle, F.E.;
 Atherosclerosis 58, 277-289, 1985
 A/Title: Molecular cloning of human LDL apolipoprotein B cDNA. Evidence for more than on
 A/Reference number: A90084; MUID:86130855; PMID:3841481
 A/Accession: A23287
 A/Molecule type: mRNA
 A/Residues: 3846-4298 <SHO>
 R/Note: Piltzner, R.; Magener, R.; Stoffel, W.
 Biol. Chem. Hoppe-Seyler 367, 1077-1083, 1986
 A/Title: Isolation, expression and characterization of a human apolipoprotein B 100-spec
 A/Reference number: A25572; MUID:87076044; PMID:3024665
 A/Accession: A25572
 A/Molecule type: mRNA
 A/Residues: 4219-4337, 'S', '4339-4563' <PFI>
 A/Cross-references: GB:M36676
 R/Note: C.F.; Chen, S.H.; Yang, C.Y.; Marcel, Y.L.; Milne, R.W.; Li, W.H.; Sparrow, J.T.;
 Proc. Natl. Acad. Sci. U.S.A. 82, 7265-7269, 1985
 A/Reference number: A24738; MUID:86042646; PMID:2932736
 A/Accession: A24738
 A/Molecule type: mRNA
 A/Residues: 'N', '3729-3731', 'T', '3733-3875', 'A', '3877-3948', 'F', '3950-3963', 'Y', '3965-3982', 'S', '39
 A/Cross-references: GB:M12413; NID:9178735; PIDN:AAA51742.1; PID:9178736
 R/Note: Chen, S.H.; Habb, G.; Yang, C.Y.; Gu, Z.W.; Lee, B.R.; Weng, S.; Silbermann, S.R.; Cai
 Science 238, 363-366, 1987
 A/Title: Apolipoprotein B-48 is the product of a messenger RNA with an organ-specific in
 A/Reference number: A40133; MUID:88018019; PMID:3659919

A/Accession: B40133
 A/Molecule type: mRNA
 A/Residues: 2155-2179 <CH1>
 A/Cross-references: GB:M18036; NID:9178799; PIDN:AAA51754.1; PID:9178800
 R/Note: this mRNA includes the stop codon of the organ-specific mRNA for apo48
 A/Accession: A40133
 A/Molecule type: protein
 A/Residues: 51-75, 101-110, 129-139, 158-174, 197-207, 276-287, 298-304, 306-314, 526-532, 538-5
 36, 1186-1498, 1537-1556, 1563-1572, 1601-1610, 1647-1661, 1697-1724, 1770-1781, 1859-1857, 1968
 A/Note: these fragments were derived from apo48
 R/Note: Hardman, D.A.; Procter, A.A.; Schilling, J.W.; Kane, J.P.
 Biochem. Biophys. Res. Commun. 149, 1214-1219, 1987
 A/Title: Carboxyl terminal analysis of human B-48 protein confirms the novel mechanism
 A/Reference number: A28002; MUID:88106542; PMID:342612
 A/Accession: A28002
 A/Molecule type: mRNA
 A/Residues: 2129-2179, 2181-2235 <HA2>
 A/Cross-references: GB:M18471
 A/Experimental source: Intestine
 A/Note: this mRNA from intestine includes a stop codon created by RNA editing in place o
 R/Note: Mehrlan, M.; Schumaker, V.N.; Fares, G.C.; West, R.; Johnson, D.F.; Kirchgessner,
 Nucleic Acids Res. 13, 6937-6953, 1985
 A/Title: Human apolipoprotein B. Identification of cDNA clones and characterization of
 A/Reference number: A24269; MUID:86041888; PMID:3903660
 A/Accession: A24269
 A/Molecule type: mRNA
 A/Residues: 3056-3159 <MRH>
 A/Cross-references: GB:X03045; NID:928783; PIDN:CAA26850.1; PID:9292609
 R/Note: Procter, A.V.; Higuchi, K.; Law, S.W.; Meglin, N.; Brewer Jr., H.B.
 Biochem. Biophys. Res. Commun. 148, 276-285, 1987
 A/Title: Identification of a novel in-frame translational stop codon in human intestine
 A/Reference number: A29659; MUID:88049670; PMID:2445342
 A/Accession: A29659
 A/Molecule type: mRNA
 A/Residues: 2169-2179 <HOS>
 A/Note: the sequence shown represents the carboxyl end of apolipoprotein B-48
 A/Note: two RNA species, 14.1kb and 7.5kb in length, were isolated from the human intest
 ch encodes the 250K apoB-48, CAA encoding 2180-Gln is substituted by the stop codon TAA
 R/Note: Yang, C.; Kim, T.W.; Meng, S.; Lee, B.; Yang, M.; Gotto Jr., A.M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 5523-5527, 1990
 A/Title: Isolation and characterization of sulfhydryl and disulfide peptides of human ap
 A/Reference number: A35783; MUID:90319144; PMID:2115173
 A/Accession: A35783
 A/Molecule type: protein
 A/Residues: 28-41, 76-97, 'I', '99-100', '175-193', '206-215', '239-249', '259-266', '357-399', '455-490', '512-5
 A/Note: Cysteines at positions 1112, 1422, 1505, 1662, 3761, 3917, and 4217 have free su
 R/Note: Liebowitz, R.C.; Miller, C.; Shively, J.E.; Schumaker, V.N.; Balla, M.A.; Lueis, A.O.
 FEBS Lett. 170, 105-108, 1984
 A/Title: Human apolipoprotein B: partial amino acid sequence.
 A/Reference number: A22006; MUID:84208786; PMID:6373369
 A/Accession: A22006
 A/Molecule type: protein
 A/Residues: 873-897, 'K', '894-896' <LE1>
 A/Accession: B22006
 A/Molecule type: protein
 A/Residues: 3113, 'L', '3115-3130', 'R', '3133-3133', 'P', '3135-3136', 'R', '3136-3136' <LE2>
 R/Note: Blackhart, B.D.; Ludwig, E.M.; Pictor, V.R.; Galati, L.; Onasch, M.A.; Wallis, S.C.;
 J. Biol. Chem. 261, 15364-15367, 1986
 A/Title: Structure of the human apolipoprotein B gene.
 A/Reference number: A92564; MUID:87057153; PMID:2946672
 A/Accession: A92564
 A/Molecule type: gene structure
 R/Note: Magener, R.; Piltzner, R.; Stoffel, W.
 Biol. Chem. Hoppe-Seyler 366, 419-425, 1987
 A/Title: Studies on the organization of the human apolipoprotein B gene.
 A/Reference number: A80715; MUID:87271140; PMID:2886136
 A/Accession: A80715
 A/Molecule type: gene structure
 R/Note: Weisgraber, K.H.; Ball Jr., S.C.
 J. Biol. Chem. 262, 11097-11103, 1987
 A/Title: Human apolipoprotein B-100 heparin-binding sites.
 A/Reference number: A92605; MUID:87280197; PMID:3301850
 A/Accession: A92605
 A/Molecule type: heparin binding and disulfide bond

R:Daehli, N.; Lee, D.M.; Mok, T.
Biochem. Biophys. Res. Commun. 137, 493-499, 1986
A:Title: Apolipoprotein B is a calcium binding protein.
A:Reference number: A90125; MUID:86242245; PMID:3087360
A:Contents: annotation; calcium binding
R:Carlsson, P.; Olofsson, S.O.; Bondjers, G.; Darnfors, C.; Wiklund, O.; Bjursell, G.
Nucleic Acids Res. 13, 8813-8826, 1985
A:Title: Molecular cloning of human apolipoprotein B cDNA.
A:Reference number: 137178; MUID:86093680; PMID:3841204
A:Accession: 137180

Query Match 95.2%; Score 60; DB 1; Length 4563;
Best Local Similarity 90.9%; Pred. No. 0.063;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KAEYKKNKRRH 11
Db 3174 KAEYKKNKRRH 3184

RESULT 2

apolipoprotein B - crab-eating macaque (fragment)
C:Species: Macaca fascicularis (crab-eating macaque)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S32802
R:Pape, M.E.; Casale, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.E.; Marotti, K.R.; Melchic
Biochim. Biophys. Acta 1086, 326-334, 1991
A:Title: Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional re
A:Reference number: S32802; MUID:92075708; PMID:1742325
A:Accession: S32802
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-596 <PAP>
A:Cross-references: UNIPROT:Q28473; EMBL:X15737; NID:G38047; PIDN:CAA33755.1; PID:G93012
C:Superfamily: apolipoprotein B

Query Match 85.7%; Score 54; DB 2; Length 596;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KAEYKKNKRRH 11
Db 15 KAEYKKNKRRH 25

RESULT 3

apolipoprotein B-100 - golden hamster (fragment)
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: C60950
R:Law, A.; Scott, J.
J. Lipid Res. 31, 1109-1120, 1990
A:Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL
A:Reference number: A60950; MUID:90324804; PMID:2373961
A:Accession: C60950
A:Molecule type: DNA
A:Residues: 1-269 <LAW>
A:Cross-references: UNIPROT:Q60537; UNIPROT:Q60536
C:Superfamily: apolipoprotein B
C:Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;

Query Match 76.2%; Score 48; DB 2; Length 269;
Best Local Similarity 72.7%; Pred. No. 0.56;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KAEYKKNKRRH 11
Db 9 KAEYKKNKRRH 19

RESULT 4

JH0102
apolipoprotein B - golden hamster (fragment)
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: JH0102
R:Smith, T.J.
submitted to GenBank, June 1990
A:Reference number: A38864
A:Accession: JH0102
A:Molecule type: DNA
A:Residues: 1-779 <SMI>
A:Cross-references: UNIPROT:Q60536; GB:M35187
A>Note: this is a revision to the sequence from reference JH0101
R:Smith, T.J.; Hautamaa, D.; Maeda, N.
Gene 87, 309-310, 1990
A:Title: Sequence of the putative low-density lipoprotein receptor-binding regions of ap
A:Reference number: JH0101; MUID:90236327; PMID:2332175
A:Contents: annotation
A>Note: this sequence has been revised in reference A38864
C:Genetics:
A:Gene: apob
C:Superfamily: apolipoprotein B
C:Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
F:646-656/Region: receptor binding

Query Match 76.2%; Score 48; DB 2; Length 779;
Best Local Similarity 72.7%; Pred. No. 1.5;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KAEYKKNKRRH 11
Db 435 KAEYKKNKRRH 445

RESULT 5

apolipoprotein B - pig (fragments)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: J70382; I46567; I46568
R:Maeda, N.; Ebert, D.L.; Doerr, T.M.; Newman, M.; Hasler-Rapacz, J.; Attie, A.D.; Rapac
Gene 70, 213-229, 1988
A:Title: Molecular genetics of the apolipoprotein B gene in pigs in relation to atherosc
A:Reference number: J70382; MUID:89108006; PMID:2905687
A:Accession: J70382
A:Molecule type: DNA
A:Residues: 1-1778 <MAE>
A:Cross-references: UNIPROT:Q29020; UNIPROT:Q29433
R:Maeda, N.; Ebert, D.L.; Doerr, T.M.; Newman, M.; Hasler-Rapacz, J.O.; Attie, A.D.; Rap

A:Title: Molecular genetics of the apolipoprotein B gene in pigs in relation to atherosc
A:Reference number: I46567
A:Accession: I46567
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-8, 'S', 10-238 <MA2>
A:Cross-references: GB:M22646; NID:G164366; PIDN:AAA30996.1; PID:G164369
A:Accession: I46568
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 239-1778 <MA3>
A:Cross-references: GB:M22647; NID:G164367; PIDN:AAA30997.1; PID:G164370
C:Comment: Apolipoprotein B is the predominant protein component of the low-density lipop
C:Genetics:
A:Gene: apob
A:Introns: 39/3; 88/3; 159/2; 238/3; 1133/1; 1171/2; 1232/3
A>Note: the list of introns may be incomplete
C:Superfamily: apolipoprotein B
C:Keywords: atherosclerosis; cholesterol metabolism; LDL; lipid binding; lipoprotein

Query Match 76.2%; Score 48; DB 2; Length 1778;
Best Local Similarity 72.7%; Pred. No. 3.3;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKKKRH 11
Db 377 KAQYKKKKDKH 387

RESULT 6

I46569

apolipoprotein B - pig (fragment)

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004

C/Accession: I46569

R/Purell, C.; Maeda, N.; Ebert, D.L.; Kaiser, M.; Lund-Katz, S.; Sturley, S.L.; Kodoyiannis, J.

A/Title: Nucleotide sequence encoding the carboxyl-terminal half of apolipoprotein B from pig

A/Reference number: I46569; MUID:94014802; PMID:8409766

A/Accession: I46569

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-2629 <PUB>

A/Cross-references: UNIPROT:Q29021; GB:U11235; NID:g164371; PIDN:AAA74655.1; PID:g951375

A/Genes: APOB

A/Introns: 1984/1, 2022/2; 2083/3

C/Superfamily: apolipoprotein B

Query Match

Best Local Similarity 76.2%; Score 48; DB 2; Length 2629;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKKKRH 11

Db 1227 KAQYKKKKDKH 1237

RESULT 7

B60950

apolipoprotein B-100 - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 31-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 07-Oct-1994

C/Accession: B60950

R/Law, A.; Scott, J.

J. Lipid Res. 31, 1109-1120, 1990

A/Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL

A/Reference number: A60950; MUID:90324804; PMID:2373961

A/Accession: B60950

A/Molecule type: mRNA

A/Residues: 1-274 <LAW>

A/Note: authors translated the codon ATA for residue 8 as Val

C/Superfamily: apolipoprotein B

C/Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;

Query Match

Best Local Similarity 71.4%; Score 45; DB 2; Length 274;

Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKKKRH 11

Db 9 KAQYKKKKDKH 19

RESULT 8

A60950

apolipoprotein B-100 - rabbit (fragment)

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 31-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004

C/Accession: A60950

R/Law, A.; Scott, J.

J. Lipid Res. 31, 1109-1120, 1990

A/Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL

A/Reference number: A60950; MUID:90324804; PMID:2373961

A/Accession: A60950

A/Molecule type: mRNA

A/Residues: 1-274 <LAW>

A/Cross-references: UNIPROT:Q7M29

A/Note: authors translated the codon GAT for residue 155 as His

C/Superfamily: apolipoprotein B

C/Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;

Query Match

Best Local Similarity 68.3%; Score 43; DB 2; Length 274;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 AEYKKKKRH 11

Db 10 AKYKKKKRH 19

RESULT 9

JH0101

apolipoprotein B-100 - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

C/Accession: JH0101; S33128; D60950

R/Smith, T.D.; Hautamaa, D.; Maeda, N.

Gene 87, 309-310, 1990

A/Title: Sequence of the putative low-density lipoprotein receptor-binding regions of

A/Reference number: JH0101; MUID:90326327; PMID:2332175

A/Accession: JH0101

A/Molecule type: DNA

A/Residues: 1-784 <SMI>

A/Cross-references: UNIPROT:Q61314; GB:W35186

R/Smith, T.; Hautamaa, D.; Maeda, N.

Submitted to the EMBL Data Library, May 1989

A/Reference number: S33128

A/Accession: S33128

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-531, 'S', '533-784 <SM2>

R/Law, A.; Scott, J.

J. Lipid Res. 31, 1109-1120, 1990

A/Title: A cross-species comparison of the apolipoprotein B domain that binds to the L

A/Reference number: A60950; MUID:90324804; PMID:2373961

A/Accession: D60950

A/Molecule type: mRNA

A/Residues: 427-531, 'S', '533-700 <LAW>

C/Genetics:

A/Genes: MGI:Apob

A/Cross-references: MGI:88052

C/Superfamily: apolipoprotein B

C/Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein

F/646-656/Region: receptor binding

Query Match

Best Local Similarity 68.3%; Score 43; DB 2; Length 784;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KAEYKKKKRH 11

Db 435 KAQYKKKKDKH 445

RESULT 10

E84675

hypothetical protein At2g27670 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C/Accession: E84675

R/Hin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

eius, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: AB4420; MUID:20083487; PMID:10617197
A:Accession: B84675
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-221 <STO>
A:Cross-references: UNIPROT:Q92UM9; GB:AE002093; NID:g3860265; PIDN:AACT3033.1; GSPDB:GN
C:Genetics:
A:Gene: A12g27670
A:Map position: 2

Query Match 65.9%; Score 41.5; DB 2; Length 221;
Best Local Similarity 81.8%; Pred. No. 6.4;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Db 1 KAEYKNGRRH 11
58 KAEYKNG-HSH 67

RESULT 11
A54063
TATA-binding protein-associated factor II - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C:Accession: A54063
R:Vertizier, C.P.; Yokomori, K.; Chen, J.L.; Tjian, R.
Science 264, 933-941, 1994
A:Title: Drosophila TAF-II 150: similarity to yeast gene TSM-1 and specific binding to C
A:Reference number: A54063; MUID:94233377; PMID:8178153
A:Accession: A54063
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1213 <VER>
A:Cross-references: UNIPROT:Q24325; GB:X79243; NID:G541664; PIDN:CAAS5830.1; PID:G541665
C:Genetics:
A:Gene: FlyBase:Taf150
A:Cross-references: FlyBase:FBgn0011836

Query Match 65.1%; Score 41; DB 2; Length 1213;
Best Local Similarity 63.6%; Pred. No. 39;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 1 KAEYKNGRRH 11
1154 KKEKKGRHKA 1164

RESULT 12
S09828
hypotheetical protein UL65 - human cytomegalovirus (strain AD169)
C:Species: human cytomegalovirus, human herpesvirus 5
A:Note: host Homo sapiens (man)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: S09828
R:Chen, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Hornell, T.;
M., Bartell, B.G.
Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
A:Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus
A:Reference number: S09749; MUID:90269039; PMID:2161319
A:Accession: S09828
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-102 <CHE>
A:Cross-references: UNIPROT:P17148; EMBL:X17403; NID:G59591; PIDN:CA35380.1; PID:G17808
A:Note: this sequence was submitted to the EMBL Data Library, December 1989
A:Note: this reading frame extends between two stop codons and does not begin with a sta
C:Superfamily: cyomegalovirus tegument protein

Query Match 61.9%; Score 39; DB 2; Length 102;
Best Local Similarity 63.6%; Pred. No. 8.5;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 1 KAEYKNGRRH 11

Db 40 RAERAKTHRH 50
:||| |||

RESULT 13
T20958
hypotheetical protein F15A4.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T20958
R:Sim, M.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19350
A:Accession: T20958
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-365 <WIL>
A:Cross-references: UNIPROT:O17816; EMBL:Z81062; PIDN:CAB02945.2; GSPDB:GN00020; CESP:F1
A:Experimental source: clone F15A4
A:Gene: CESP:F15A4.1
A:Map position: 2
A:Introns: 96/1; 158/2; 210/3; 251/3; 296/2

Query Match 61.9%; Score 39; DB 2; Length 365;
Best Local Similarity 70.0%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 2 AEYKNGRRH 11
214 AVMKNGRRH 223

RESULT 14
H88337
protein F15A4.1 (imported) - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H88337
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: H88337
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-452 <STO>
A:Cross-references: UNIPROT:O17816; GB:chr_II; PIDN:CAB02945.1; PID:G3875977; GSPDB:GN00
C:Genetics:
A:Gene: F15A4.1
A:Map position: 2

Query Match 61.9%; Score 39; DB 2; Length 452;
Best Local Similarity 70.0%; Pred. No. 34;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 2 AEYKNGRRH 11
214 AVMKNGRRH 223

RESULT 15
S44617
CS0C3.11 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S44617
R:Favell, A.D.
submitted to the EMBL Data Library, May 1993
A:Description: Sequence of the C. elegans cosmid CS0C3.
A:Reference number: S44627

A:Accession: S44617
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-734 <FAV>
 A:Cross-references: UNIPROT:P34374; EMBL:L14433; NID:g289649; PID:g289650
 C:Genetics:
 A:introns: 24/2; 87/3; 175/1; 259/1; 290/3; 346/3; 460/3; 538/3

Query Match
 Best Local Similarity 61.9%; Score 39; DB 2; Length 734;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAEYKKNR 10
 :|||:||||
 Db 65 RAELKSKNR 74

Search completed: January 12, 2005, 13:31:56
 Job time : 21.2258 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2005, 12:49:11 ; Search time 109.645 Seconds
(without alignments)
57.724 Million cell updates/sec

Title: US-10-657-404A-1
Perfect score: 63
Sequence: 1 KAEYKKNKGRH 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	95.2	3262	2 Q13788	Q13788 homo sapien
2	60	95.2	4563	1 APB_HUMAN	P04114 homo sapien
3	60	95.2	4563	2 Q72600	Q72600 homo sapien
4	57	90.5	414	2 Q7YQR5	Q7YQR5 actus vocif
5	54	85.7	596	2 Q28473	Q28473 macaca fasc
6	53	84.1	364	2 Q7YQ02	Q7YQ02 oryctolopus
7	51	81.0	445	2 Q7YR14	Q7YR14 rhinolophus
8	50	79.4	304	2 Q7YQ09	Q7YQ09 echinops te
9	48	76.2	314	2 Q7YQ08	Q7YQ08 ictonyx str
10	48	76.2	316	2 Q7YQ03	Q7YQ03 nandina bi
11	48	76.2	318	2 Q7YQ09	Q7YQ09 zalophus ca
12	48	76.2	411	2 Q7YQ07	Q7YQ07 ochoiona pr
13	48	76.2	436	2 Q7YQ06	Q7YQ06 nyctimene a
14	48	76.2	438	2 Q7YQ04	Q7YQ04 balaena mys
15	48	76.2	438	2 Q7YQ04	Q7YQ04 roussetus a
16	48	76.2	440	2 Q7YQ03	Q7YQ03 tadaxida br
17	48	76.2	440	2 Q7YQ04	Q7YQ04 myotis veli
18	48	76.2	441	2 Q7YQ03	Q7YQ03 phocoenoid
19	48	76.2	443	2 Q7YQ05	Q7YQ05 megaderma l
20	48	76.2	445	2 Q7YQ06	Q7YQ06 bradypus tr
21	48	76.2	445	2 Q7YQ08	Q7YQ08 cynocephalu
22	48	76.2	445	2 Q7YQ08	Q7YQ08 chaetophrac
23	48	76.2	780	2 Q60536	Q60536 mesocricetu
24	48	76.2	780	2 Q60537	Q60537 mesocricetu
25	48	76.2	1540	2 Q29433	Q29433 sus scrofa
26	48	76.2	2629	2 Q29021	Q29021 sus scrofa
27	47	74.6	320	2 Q7YQ04	Q7YQ04 manis sp. x
28	47	74.6	322	2 Q7YQ05	Q7YQ05 manis sp. x
29	47	74.6	359	2 Q7YQ05	Q7YQ05 loxodonta a
30	47	74.6	361	2 Q7YQ04	Q7YQ04 elephas max
31	47	74.6	445	2 Q7YR13	Q7YR13 hexaprotodon

32	46	73.0	263	2 Q7YQ00	Q7YQ00 procavia ca
33	46	73.0	364	2 Q7YQ01	Q7YQ01 dugong dugo
34	45	71.4	319	2 Q7YQ00	Q7YQ00 vulpes vulp
35	45	71.4	364	2 Q7YQ03	Q7YQ03 elephantiu
36	45	71.4	392	2 Q7YR11	Q7YR11 tarsius syr
37	45	71.4	426	2 Q7YQ02	Q7YQ02 alces alces
38	45	71.4	438	2 Q7YQ07	Q7YQ07 pteropus hy
39	45	71.4	446	2 Q7YR06	Q7YR06 lama glama
40	45	71.4	4743	2 Q7YQ05	Q7YQ05 rattus norv
41	44	69.8	630	2 Q61B88	Q61B88 plasmodium
42	43	68.3	255	2 Q7YQ08	Q7YQ08 caluromys p
43	43	68.3	274	2 Q7YQ09	Q7YQ09 oryctolagus
44	43	68.3	319	2 Q7YQ02	Q7YQ02 panthera le
45	43	68.3	405	2 Q7YQ00	Q7YQ00 tachyglousu

ALIGNMENTS

RESULT 1					
ID	Q13788	PRELIMINARY:	PRT:	3262 AA.	
AC	Q13788;				
DT	01-NOV-1996 (TREMBLrel. 01, Created)				
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)				
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)				
DE	APOB protein (Fragment).				
GN	Name=APOB;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=87191999; PubMed=2883086;				
RA	Carlsson P., Darnfora C., Olofsson S.O., Bjursell G.;				
RT	"Analysis of the human apolipoprotein B gene; complete structure of				
RL	the B-74 region."				
RL	Gene 49:29-51(1986).				
DR	EMBL; M15421; AAA51758.1; -.				
DR	PIR; A27850; LPHUB.				
DR	GO; GO:0005576; C:extracellular; NAS.				
DR	GO; GO:0005319; F:lipid transporter activity; NAS.				
DR	GO; GO:0006869; P:lipid transport; NAS.				
FT	NON_TER				
FT	1				
FT	SEQUENCE 3262 AA; 370140 MW; 56603BC0618DD40D CRC64;				
Query Match		95.2%	Score 60;	DB 2;	Length 3262;
Best Local Similarity		90.9%	Pred. NO. 0.25;		
Matches 10; Conservative		1;	Mismatches	0;	Indels 0;
Matches			Gaps	0;	
QY	1 KAEYKKNKGRH 11				
DB	1873 KAEYKKNKGRH 1883				
RESULT 2					
APB_HUMAN	STANDARD:	PRT:	4563 AA.		
ID	P04114; 000502; Q13787;				
AC	P04114;				
DT	01-NOV-1986 (Rel. 03, Created)				
DT	01-NOV-1986 (Rel. 03, Last sequence update)				
DT	05-JUN-2004 (Rel. 44, Last annotation update)				
DE	Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipoprotein				
DE	B-48 (Apo B-48)].				
GN	Name=APOB;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=87016385; PubMed=3763409;				

RA Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.,
RA Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.,
RT "Complete cDNA and derived protein sequence of human apolipoprotein B-
RT 100.";
RL Nucleic Acids Res. 14:7501-7503(1986).
RP
RX
RA SEQUENCE FROM N.A., AND VARIANT GLU-4181.
RA MEDLINE=88003974; PubMed=3652907;
RA Ludwig E.H., Blackhart B.D., Pierotti V.R., Caiati L., Fortier C.,
RA Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.,
RT "DNA sequence of the human apolipoprotein B gene.";
RL DNA 6:363-372(1987).
RP
RX SEQUENCE FROM N.A., AND VARIANTS ILE-98 AND GLU-4181.
RA MEDLINE=87008488; PubMed=3759943.
RA Chen S.-H., Yang C.-Y., Chan P.-F., Setzer D., Tanimura M., Li W.-H.,
RA Goto A.M., Jr., Chan L.,
RT "The complete cDNA and amino acid sequence of human apolipoprotein B-
RT 100.";
RL J. Biol. Chem. 261:12918-12921(1986).
RP
RX SEQUENCE FROM N.A.,
RA MEDLINE=87041416; PubMed=3464946;
RA Law S.W., Grant S.M., Higuchi K., Hospattankar A.V., Lackner K.J.,
RA Lee N., Brewer H.B., Jr.,
RT "Human liver apolipoprotein B-100 cDNA: complete nucleic acid and
RT derived amino acid sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146(1986).
RP
RX SEQUENCE FROM N.A.,
RA MEDLINE=87161758; PubMed=3030729;
RA Cladatas C., Hadzopoulou-Cladaras M., Nolte R.T., Atkinson D.,
RA Zannis V.I.,
RT "The complete sequence and structural analysis of human apolipoprotein
RT B-100: relationship between apob-100 and apob-48 forms.";
RL EMBO J. 5:3495-3507(1986).
RP
RX SEQUENCE OF 709-906 FROM N.A.,
RA MEDLINE=85270450; PubMed=3860836;
RA Deeb S.S., Wolulsky A.G., Albers J.J.,
RT "A partial cDNA clone for human apolipoprotein B,"
RL Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986(1985).
RP
RX SEQUENCE OF 3056-3159 FROM N.A.,
RA MEDLINE=86041888; PubMed=3903660;
RA Mehriban M., Schumaker V.N., Fareed G.C., West R., Johnson D.F.,
RA Kirchgessner T.G., Lin H.-C., Wang X., Ma Y., Mendiaz E., Lusis A.J.,
RT "Human apolipoprotein B: identification of cDNA clones and
RT characterization of mRNA.";
RL Nucleic Acids Res. 13:6937-6953(1985).
RP
RX SEQUENCE OF 1937-2018 AND 3811-4334 FROM N.A., AND VARIANT GLU-4181.
RA MEDLINE=86093680; PubMed=3841204;
RA Carlsson P., Olofsson S.O., Bondjers G., Darnfors C., Wiklund O.,
RA Bjursell G.,
RT "Molecular cloning of human apolipoprotein B cDNA.";
RL Nucleic Acids Res. 13:8813-8826(1985).
RP
RX SEQUENCE OF 3109-4563 FROM N.A.,
RA MEDLINE=85300528; PubMed=2994225;
RA Knott T.J., Rall S.C., Jr., Innerarity T.L., Jacobson S.F., Urdia M.S.,
RA Levy-Wilson B., Powell L.M., Pease R.J., Eddy R., Nakai H., Byers M.,
RA Priestley L.M., Robertson E., Rall L.B., Betsholtz C., Shows T.B.,
RT "Human apolipoprotein B: structure of carboxyl-terminal domains, sites
RT of gene expression, and chromosomal localization.";
RL Science 230:37-43(1985).
RP
RX SEQUENCE OF 1-291 FROM N.A.,
RA MEDLINE=86149325; PubMed=3511177;
RA Procter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V.,
RA Chen G.C., Kirsner S.W., McIntire G., Kane J.P.,
RT "Isolation of a cDNA clone encoding the amino-terminal region of human
RT apolipoprotein B.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:1467-1471(1986).
RP
RX SEQUENCE OF 1-1670 FROM N.A., AND VARIANT ILE-98.
RA MEDLINE=86287319; PubMed=3461454;
RA Procter A.A., Hardman D.A., Sato K.Y., Schilling J.W., Yamanaka M.,
RA Hott V.J., Herrild K.A., Chen G.C., Kane J.P.,
RT "Analysis of cDNA clones encoding the entire B-26 region of human
RT apolipoprotein B.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682(1986).
RP
RX PARTIAL SEQUENCE, AND IDENTIFICATION OF APO-B48.
RA MEDLINE=88018019; PubMed=3659919;
RA Chen S.-H., Habib G., Yang C.-H., Gu Z.-W., Lee B.R., Weng S.-H.,
RA Silbermann S.R., Gal S.-O., Deslypere J.P., Rosseneu M.,
RA Goto A.M., Jr., Li W.-H., Chan L.,
RT "Apolipoprotein B-48 is the product of a messenger RNA with an organ-
RT specific in-frame stop codon.";
RL Science 238:363-366(1987).
RP
RX DOMAINS.
RA MEDLINE=87039351; PubMed=3773997;
RA Knott T.C., Pease R.J., Powell L.M., Wallis S.C., Rall S.C., Jr.,
RA Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R.,
RA Johnson D., Fuller M., Lusis A.J., McCarthy B.J., Mahley R.W.,
RT "Complete protein sequence and identification of structural domains of
RT human apolipoprotein B.";
RL Nature 323:734-738(1986).
RP
RX DOMAINS.
RA Yang C.-Y., Chen S.-H., Gianturco S.H., Bradley W.A., Sparrow J.T.,
RA Tanimura M., Li W.-H., Sparrow D.A., DeLoof H., Rosseneu M.,
RA Lee F.-S., Gu Z.-W., Goto A.M., Jr., Chan L.,
RT "Sequence, structure, receptor-binding domains and internal repeats of
RT human apolipoprotein B-100.";
RL Nature 323:738-742(1986).
RP
RX CALCULUM-BINDING DATA.
RA MEDLINE=86242245; PubMed=3087360;
RA Dashi N., Lee D.M., Mok T.,
RT "Apolipoprotein B is a calcium binding protein.";
RL Biochem. Biophys. Res. Commun. 137:493-499(1986).
RP
RX PALMITOYLATION OF CY3-1112.
RA MEDLINE=20143590; PubMed=10679026;
RA Zhao Y., McCabe J.B., Vance J., Berthiaume L.G.,
RT "Palmitoylation of apolipoprotein B is required for proper
RT intracellular sorting and transport of cholesterol esters and
RT triglycerides.";
RL Mol. Biol. Cell 11:721-734(2000).
RP
RX VARIANT SER-4338.
RA MEDLINE=91071750; PubMed=1979313;
RA Navajas M., Laurent A.-M., Moreel J.-F., Ragab A., Cambou J.-P.,
RA Cuny G., Cambien F., Roizes G.,
RT "Detection by denaturing gradient gel electrophoresis of a new
RT polymorphism in the apolipoprotein B gene.";
RL Hum. Genet. 86:91-93(1990).
RP
RX VARIANT FDB GLN-3527.
RA MEDLINE=89098975; PubMed=2563166;
RA Soria L.F., Ludwig E.H., Clarke H.R.G., Vega G.L., Grundy S.M.,
RA McCarthy B.J.,
RT "Association between a specific apolipoprotein B mutation and familial
RT defective apolipoprotein B-100.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).
RP
RX VARIANT LEU-2739.
RA MEDLINE=91016974; PubMed=2216805;
RA Huang L.-S., Gavish D., Breslow J.L.,
RT "Sequence polymorphism in the human apob gene at position 8344.";
RL Nucleic Acids Res. 18:5922-5922(1990).

RN [20]
 RP VARIANT FDB CYS-3558.
 RX MEDLINE=95190020; PubMed=7883971;
 RA Pullinger C.R., Hennessy L.K., Chatterton J.E., Liu W., Love J.A.,
 RA Mendel C.M., Frost P.H., Malloy M.J., Schumaker V.N., Kane J.P.;
 RT "Familial ligand-defective apolipoprotein B. Identification of a new
 RT mutation that decreases LDL receptor binding affinity.";
 RL J. Clin. Invest. 95:1225-1234(1995).
 RN [21]
 RP VARIANTS LEU-1437; SER-1914; LYS-2566; THR-3121; ALA-3945; MET-4128
 RP AND THR-4481.
 RX MEDLINE=97044521; PubMed=8889592;
 RA Poirier O., Ricard S., Behague I., Souriau C., Evans A.E.,
 RA Arveiler D., Marques-Vidal P., Luc G., Roizes G., Cambien F.;
 RT "Detection of new variants in the apolipoprotein B (Apo B) gene by
 RT PCR-SSCP.";
 RL Hum. Mutat. 8:282-285(1996).
 RN [22]
 RP VARIANTS FDB GLN-3527 AND CYS-3558.
 RX MEDLINE=97403938; PubMed=9259199;
 RA Rabes J.P., Varret M., Saint-dore B., Erlich D., Jondeau G.,
 RA Ktempf M., Graudet P., Junien C., Boileau C.;
 RT "Familial ligand-defective apolipoprotein B-100: simultaneous
 RT detection of the ARG3500-->GLN and ARG3511-->CYS mutations in a French
 RT population.";
 RL Hum. Mutat. 10:160-163(1997).
 RN [23]
 RP VARIANTS SER-1914; ARG-1923; LEU-2739; ASP-3319; THR-3427; GLN-3432
 RP AND ILE-3921.
 RX MEDLINE=98141125; PubMed=9490296;
 RA Leren T.P., Bakken K.S., Hoel V., Hjermann I., Berg K.;
 RT "Screening for mutations of the apolipoprotein B gene causing
 RT hypochlolesterolemia.";
 RL Hum. Genet. 102:44-49(1998).
 CC -1- FUNCTION: Apolipoprotein B is a major protein constituent of
 CC chylomicrons (apo B-48), LDL (apo B-100) and VLDL (apo B-100). Apo
 CC B-100 functions as a recognition signal for the cellular binding
 CC and internalization of LDL particles by the apoB/E receptor.
 CC -1- SUBCELLULAR LOCATION: Secreted.

Query Match 95.2%; Score 60; DB 1; Length 4563;
 Best Local Similarity 90.9%; Pred. No. 0.36;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKKNKGRH 11
 DB 3174 KAOYKKNKGRH 3184

RESULT 3
 Q72600 PRELIMINARY; PRT; 4563 AA.
 AC Q72600;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Apolipoprotein B (Including Ag(X) antigen).
 OS Name=APOB;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
 RA Ahearn M.O., Kuidanek S.A., Rajkumar N., Toth E.J., Yi Q.,
 RA Nickerson D.A.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AY344608; AAF72970.1; --
 DR GO; GO:0005319; P:lipid transporter activity; IEA.
 DR GO; GO:0006869; P:lipid transport; IEA.
 DR InterPro; IPR009454; DUF1081.
 DR InterPro; IPR001747; Lipid_transport_N.

DR Pfam; PF06448; DUF1081; 1.
 DR Pfam; PF01347; Vitellinogen_N; 1.
 DR SMART; SM00638; LPD_N; 1.
 KW Lipoprotein.
 SQ SEQUENCE 4563 AA; 515553 MW; 030B34167CEDC63C CRC64;

Query Match 95.2%; Score 60; DB 2; Length 4563;
 Best Local Similarity 90.9%; Pred. No. 0.36;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKKNKGRH 11
 DB 3174 KAOYKKNKGRH 3184

RESULT 4
 Q7YOR5 PRELIMINARY; PRT; 414 AA.
 AC Q7YOR5;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Apolipoprotein B 100 (Fragment).
 GN Name=APOB-100;
 OS Aotus vociferans (Spix's owl monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 OC NCBI_TaxID=57176;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22761261; PubMed=12878460;
 RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
 RT "A new phylogenetic marker, apolipoprotein B, provides compelling
 RT evidence for eutherian relationships.";
 RL Mol. Phylogenet. Evol. 28:225-240(2003).
 DR EMBL; AF548396; AAP97352.1; --
 KW Lipoprotein.
 FT NON_TER 1 1
 FT NON_TER 414 414
 SQ SEQUENCE 414 AA; 45955 MW; EEPFA8492157E1BDE CRC64;

Query Match 90.5%; Score 57; DB 2; Length 414;
 Best Local Similarity 81.8%; Pred. No. 0.095;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKKNKGRH 11
 DB 47 KAOYKKNKGRH 57

RESULT 5
 Q28473 PRELIMINARY; PRT; 596 AA.
 AC Q28473;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Apolipoprotein B (Fragment).
 OS Macaca fascicularis (Cray eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OC NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP TISSUE=Liver;
 RX MEDLINE=92075708; PubMed=1742325;
 RA Pape M.E., Castle C.K., Murray R.W., Funk G.M., Hunt C.E.,
 RA Marotti K.R., Welch G.W.;
 RT "Apo B metabolism in the cynomolgus monkey: evidence for post-
 RT transcriptional regulation.";
 RL Biochim. Biophys. Acta 1086:326-334(1991).
 RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Murray R.;

RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.

DR EMBL: X15137; CA3375.1; -.

DR PIR: S32802; S32802.

KM Lipoprotein.

FT NON_TER 1

FT NON_TER 596

SO SEQUENCE 596 AA; 66757 MW; B13BA74E25C3120 CRC64;

Query Match 85.7%; Score 54; DB 2; Length 596;

Best Local Similarity 81.8%; Pred. No. 0.48;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
DB 15 KAQYKKNKRRH 25

RESULT 6

ID 07Y002 PRELIMINARY; PRT; 364 AA.

AC 07Y002; 01-OCT-2003 (TRENBLrel. 25, Created)

DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)

DE Apolipoprotein B 100 (Fragment).

GN Name=apob-100;

OS Oryctolagus afer (Aardvark).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Tubulidentata; Orycteropodidae; Orycterops.

OC NCBI_Taxid=9818;

RP SEQUENCE FROM N.A.

RA MEDLINE=22761261; PubMed=12878460;

RT "A new phylogenetic marker, apolipoprotein B, provides compelling

RL evidence for eutherian relationships."

DR EMBL: AF548409; AAP97365.1; -.

KM Lipoprotein.

FT NON_TER 1

FT NON_TER 364

SO SEQUENCE 364 AA; 40532 MW; 163C27D76ED858DD CRC64;

Query Match 84.1%; Score 53; DB 2; Length 364;

Best Local Similarity 81.8%; Pred. No. 0.43;

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
DB 76 KAQYKKNKRRH 86

Query Match 84.1%; Score 53; DB 2; Length 364;

Best Local Similarity 81.8%; Pred. No. 0.43;

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 7

ID 07YR14 PRELIMINARY; PRT; 445 AA.

AC 07YR14; 01-OCT-2003 (TRENBLrel. 25, Created)

DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)

DE Apolipoprotein B (Fragment).

GN Name=apob-100;

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Rhinolophidae;

OC Rhinolophinae; Rhinolophus.

OC NCBI_Taxid=178895;

RP SEQUENCE FROM N.A.

RA MEDLINE=22761261; PubMed=12878460;

RT "A new phylogenetic marker, apolipoprotein B, provides compelling

RL evidence for eutherian relationships."

DR EMBL: AF548409; AAP97365.1; -.

KM Lipoprotein.

FT NON_TER 1

FT NON_TER 596

SO SEQUENCE 596 AA; 66757 MW; B13BA74E25C3120 CRC64;

Query Match 85.7%; Score 54; DB 2; Length 596;

Best Local Similarity 81.8%; Pred. No. 0.48;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
DB 15 KAQYKKNKRRH 25

Query Match 85.7%; Score 54; DB 2; Length 596;

Best Local Similarity 81.8%; Pred. No. 0.48;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RT evidence for eutherian relationships."

RL Mol. Phylogenet. Evol. 28:225-240(2003).

DR EMBL: AY243371; AAP50759.1; -.

DR Lipoprotein.

FT NON_TER 1

FT NON_TER 445

SO SEQUENCE 445 AA; 49395 MW; 6ECCAB23CB347E73 CRC64;

Query Match 81.0%; Score 51; DB 2; Length 445;

Best Local Similarity 81.8%; Pred. No. 1.2;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
DB 76 KAQYKKNKRRH 86

Query Match 81.0%; Score 51; DB 2; Length 445;

Best Local Similarity 81.8%; Pred. No. 1.2;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
DB 76 KAQYKKNKRRH 86

Query Match 81.0%; Score 51; DB 2; Length 445;

Best Local Similarity 81.8%; Pred. No. 1.2;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
DB 76 KAQYKKNKRRH 86

Query Match 81.0%; Score 51; DB 2; Length 445;

Best Local Similarity 81.8%; Pred. No. 1.2;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
DB 76 KAQYKKNKRRH 86

Query Match 81.0%; Score 51; DB 2; Length 445;

Best Local Similarity 81.8%; Pred. No. 1.2;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
DB 76 KAQYKKNKRRH 86

Query Match 81.0%; Score 51; DB 2; Length 445;

Best Local Similarity 81.8%; Pred. No. 1.2;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
DB 76 KAQYKKNKRRH 86

Query Match 81.0%; Score 51; DB 2; Length 445;

Best Local Similarity 81.8%; Pred. No. 1.2;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
DB 76 KAQYKKNKRRH 86

Query Match 81.0%; Score 51; DB 2; Length 445;

Best Local Similarity 81.8%; Pred. No. 1.2;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
DB 76 KAQYKKNKRRH 86

Query Match 81.0%; Score 51; DB 2; Length 445;

Best Local Similarity 81.8%; Pred. No. 1.2;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
DB 76 KAQYKKNKRRH 86

Query Match 81.0%; Score 51; DB 2; Length 445;

Best Local Similarity 81.8%; Pred. No. 1.2;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
DB 76 KAQYKKNKRRH 86

Query Match 81.0%; Score 51; DB 2; Length 445;

Best Local Similarity 81.8%; Pred. No. 1.2;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
DB 76 KAQYKKNKRRH 86

Query Match 81.0%; Score 51; DB 2; Length 445;

Best Local Similarity 81.8%; Pred. No. 1.2;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
DB 76 KAQYKKNKRRH 86

Query Match 81.0%; Score 51; DB 2; Length 445;

Best Local Similarity 81.8%; Pred. No. 1.2;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
DB 76 KAQYKKNKRRH 86

Query Match 81.0%; Score 51; DB 2; Length 445;

Best Local Similarity 81.8%; Pred. No. 1.2;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
DB 76 KAQYKKNKRRH 86

Query Match 81.0%; Score 51; DB 2; Length 445;

Best Local Similarity 81.8%; Pred. No. 1.2;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
DB 76 KAQYKKNKRRH 86

Query Match 81.0%; Score 51; DB 2; Length 445;

Best Local Similarity 81.8%; Pred. No. 1.2;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
DB 76 KAQYKKNKRRH 86

Query Match 81.0%; Score 51; DB 2; Length 445;

RESULT 13		07YQM8	
ID	Q7YQM8	PRELIMINARY:	PRT: 436 AA.
AC	Q7YQM8;		
DT	01-OCT-2003 (TrEMBLrel. 25, Created)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Apolipoprotein B 100 (Fragment).		
GN	Name=apob-100;		
OS	Nyctimene albigenter (Common tube-nosed fruit bat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;		
OC	Pteropodinae; Nyctimene.		
OX	NCBI_Taxid=48988;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22761261; Pubmed=12878460;		
RA	Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;		
RT	"A new phylogenetic marker, apolipoprotein B, provides compelling		
RT	evidence for eutherian relationships.";		
RL	Mol. Phylogenet. Evol. 28:225-240(2003).		
DR	EMBL; AF548435; AAP97391.1, -.		
KM	Lipoprotein.		
FT	NON_TER 1 1		
FT	NON_TER 436 436		

SQ SEQUENCE 436 AA; 48717 MM; 1CA7EAD72D2C629 CRC64;
 Query Match 76.2%; Score 48; DB 2; Length 436;
 Best Local Similarity 72.7%; Pred. No. 4.1;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KAEYKKNKRRH 11
 ||:|||||:
 Db 76 KAQYKKNKDKH 86

Query Match 76.2%; Score 48; DB 2; Length 436;
 Best Local Similarity 72.7%; Pred. No. 4.1;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KAEYKKNKRRH 11
 ||:|||||:
 Db 76 KAQYKKNKDKH 86

Search completed: January 12, 2005, 13:30:53
 Job time : 110.645 secs

RESULT 14
 Q7YR4
 ID Q7YR4 PRELIMINARY; PRT; 438 AA.
 AC Q7YR4;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Apolipoprotein B 100 (Fragment).
 GN Name=apOB-100;
 OS Balaena mysticetus (Bowhead whale).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti; Balenidae;
 OC Balaena.
 OX NCBI_TaxID=27602;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA MEDLINE=22761261; PubMed=12878460;
 RA Amrine-Madsen H.; Koepfli K.-P.; Wayne R.K.; Springer M.S.;
 RT "A new phylogenetic marker, apolipoprotein B, provides compelling
 RL evidence for eutherian relationships."
 RL Mol. Phylogenet. Evol. 28:225-240(2003).
 DR EMBL; AF548397; AAP97353.1; -.
 KW Lipoprotein.
 FT NON_TER 1
 FT NON_TER 438
 SQ SEQUENCE 438 AA; 48849 MM; 48984F295035ADD0 CRC64;

Query Match 76.2%; Score 48; DB 2; Length 438;
 Best Local Similarity 72.7%; Pred. No. 4.1;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAEYKKNKRRH 11
 ||:|||||:
 Db 71 KAQYKKNKDKH 81

RESULT 15
 Q7YR04
 ID Q7YR04 PRELIMINARY; PRT; 438 AA.
 AC Q7YR04;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Apolipoprotein B (Fragment).
 OS Roussetus amplexicaudatus (Common roussette).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
 OC Pteropodinae; Roussetus.
 OX NCBI_TaxID=58083;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA MEDLINE=22761261; PubMed=12878460;
 RA Amrine-Madsen H.; Koepfli K.-P.; Wayne R.K.; Springer M.S.;
 RT "A new phylogenetic marker, apolipoprotein B, provides compelling
 RL evidence for eutherian relationships."
 RL Mol. Phylogenet. Evol. 28:225-240(2003).
 DR EMBL; AY243383; AAP50771.1; -.
 KW Lipoprotein.
 FT NON_TER 1
 FT NON_TER 438
 SQ SEQUENCE 438 AA; 48597 MM; 41C890DEAF95C872 CRC64;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2005, 12:47:25 : Search time 101.484 Seconds
(without alignments)
38.883 Million cell updates/sec

Title: US-10-657-404A-2
Perfect score: 54
Sequence: 1 TTRLTRKRGK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues
Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	54	100.0	11 2 AAW57205	AAW57205 Apo B bin
2	54	100.0	13 2 AAW57207	AAW57207 Apo B 100
3	54	100.0	15 2 AAW56892	AAW56892 ApoB-100
4	54	100.0	20 6 AB037575	AB037575 Heparin b
5	54	100.0	22 2 AAW57208	AAW57208 Apo B 100
6	54	100.0	22 2 AAW57209	AAW57209 Apo B 100
7	54	100.0	34 5 AAE14541	AAE14541 Human apo
8	54	100.0	36 2 AAW56876	AAW56876 Nucleic a
9	54	100.0	37 2 AAW64587	AAW64587 Human apo
10	54	100.0	51 2 AAW56845	AAW56845 Nucleic a
11	54	100.0	343 4 ABB37687	ABB37687 Peptide #
12	54	100.0	343 4 ABG52504	ABG52504 Human liv
13	54	100.0	377 2 AAR72704	AAR72704 Human apo
14	54	100.0	377 2 AAR34031	AAR34031 Sequence
15	54	100.0	2463 8 AD037400	AD037400 Human apo
16	54	100.0	3923 8 AAY31337	AAY31337 Human apo
17	54	100.0	4536 2 AAW41262	AAW41262 Apolipop
18	54	100.0	4536 2 AAW96826	AAW96826 Amino aci
19	54	100.0	4560 5 AAU98981	AAU98981 Human apo
20	54	100.0	4561 7 ADD48677	ADD48677 Human pro
21	54	100.0	4563 5 AAO15893	AAO15893 Human apo
22	54	100.0	4563 6 ABR40253	ABR40253 Human a1
23	54	100.0	4563 6 ABU79140	ABU79140 Apolipop
24	54	100.0	4563 7 ADF43408	ADF43408 Apolipop
25	54	100.0	4563 8 ADH18871	ADH18871 Human apo

26	54	100.0	4563 8 ADH18870	ADH18870 Human apo
27	54	100.0	4563 8 ADO33445	ADO33445 Human apo
28	54	100.0	4563 8 ADO33447	ADO33447 Human apo
29	54	100.0	4590 4 AAO33184	AAO33184 Novel hum
30	49	90.7	15 2 AAW41261	AAW41261 Apolipop
31	45	83.3	10 2 AAY30682	AAY30682 Apo-B100
32	45	83.3	10 2 AAY30687	AAY30687 Apo-B100
33	45	83.3	10 4 AAG94401	AAG94401 Human com
34	45	83.3	10 4 AAG94535	AAG94535 Human com
35	45	83.3	10 4 AAG94441	AAG94441 Human com
36	44	81.5	10 2 AAY30690	AAY30690 Apo-B100
37	44	81.5	10 2 AAY30692	AAY30692 Apo-B100
38	44	81.5	10 2 AAY30686	AAY30686 Apo-B100
39	44	81.5	10 2 AAY30688	AAY30688 Apo-B100
40	44	81.5	11 2 AAW57206	AAW57206 Apo B 100
41	44	81.5	11 2 AAW87717	AAW87717 Analogue
42	44	81.5	11 5 AAE21732	AAE21732 BSMR effe
43	44	81.5	11 6 ABU07938	ABU07938 Apoprotei
44	44	81.5	11 7 ADF56451	ADF56451 Human apo
45	44	81.5	12 2 AAW41260	AAW41260 Apolipop

ALIGNMENTS

RESULT 1
AAW57205 standard; peptide, 11 AA.

AAW57205; (first entry)

03-AUG-1998

Apo B binding site peptide 2.

Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.

Synthetic.

WO9813385-A2.

02-APR-1998.

25-SEP-1997; 97WO-GB002610.

27-SEP-1996; 96GB-00020153.

(UYST) UNIV STRATHCLYDE.

Halbert GW, Owens MD, Baillie G;
WPI, 1998-230637/20.

Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.

Claim 12; Page 52; 73pp; English.

The present sequence represents a specifically claimed Apo B binding site peptide which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KAEIKKKRKH (1) or TTRLTRKRGK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring,

CC receptor-competent LDL particles do not require the complete apo B
 CC sequence, which is large and tends to aggregate, to provide binding
 CC affinity to an apo B protein receptor
 XX
 SQ Sequence 11 AA;

Query Match
 Best Local Similarity 100.0%; Score 54; DB 2; Length 11;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 TTRLTRKRGK 11
 1 TTRLTRKRGK 11

RESULT 2
 AAW57207
 ID AAW57207 standard; peptide; 13 AA.
 AC AAW57207;
 XX
 XX 03-AUG-1998 (first entry)
 DT
 XX

DE Apo B 100 binding site peptide analogue peptide B.
 XX Apo B; binding site; receptor; cancer; drug delivery; anticancer;
 KM growth supplement; non-natural lipid particle; low density lipoprotein;
 KM LDL; receptor component; apo B100 receptor site.
 XX
 OS Synthetic.

FT Key Location/Qualifiers
 FT Modified-site 1 /note= "attached to retinoic acid"
 XX
 XX WO9813385-A2.
 XX
 PD 02-APR-1998.
 XX
 XX 25-SEP-1997; 97WO-GB002610.
 XX
 PR 27-SEP-1996; 96GB-00020153.
 XX
 PA (UYST) UNIV STRATHCLYDE.
 XX
 PI Halbert GW, Owens MD, Baillie G;
 XX
 DR WPI; 1998-230637/20.
 XX

PT Non-natural lipid particle comprising peptide binding to apo B protein
 PT receptor - useful as, e.g. vector for delivering drugs to cancer cells
 PT that express this receptor.
 XX
 PS Claim 13; Fig 7; 73pp; English.

CC The present sequence represents a specifically claimed Apo B 100 binding
 CC site peptide analogue which can be used as a component of a non-
 CC naturally occurring, receptor-competent low density lipoprotein (LDL)
 CC particle of the present invention. The LDL particle comprises at least 1
 CC peptide component that has at least 1 binding site for an apo B protein
 CC receptor and at least 1 lipophilic substituent. Also described in the
 CC invention are peptides containing an apo B binding sequence with at least
 CC 70% identity with sequences: KAEYKNKRRH (1) or TTRLTRKRGK (2), or their
 CC dimers. Non-naturally occurring, receptor-competent LDL particles are
 CC useful as: (i) drug-targeting vectors for delivering anticancer drugs to
 CC cancer cells that express an apo B protein receptor, and (ii) additives
 CC for cell culture media especially as growth supplements. Non-naturally
 CC occurring, receptor-competent LDL particles do not require the complete
 CC apo B sequence, which is large and tends to aggregate, to provide binding
 CC affinity to an apo B protein receptor
 XX
 SQ Sequence 13 AA;

Query Match
 Best Local Similarity 100.0%; Score 54; DB 2; Length 13;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TTRLTRKRGK 11
 2 TTRLTRKRGK 12

RESULT 3
 AAW6892
 ID AAW6892 standard; peptide; 15 AA.
 AC AAW6892;
 XX
 XX 22-APR-1999 (first entry)
 DT
 XX

DE Apob-100 nuclear localisation signal sequence, residues 3353-3367.
 XX Human apolipoprotein B-100; apob-100; very-low density lipoprotein; VLDL;
 KM apolipoprotein; binding; in vivo transport; nucleic acid; binding domain;
 KM nuclear localisation sequence; gene therapy; cancer; cystic fibrosis;
 XX non-small cell lung carcinoma; diabetes; arteriosclerosis.
 OS Homo sapiens.

XX
 XX WO9856938-A1.
 XX
 PD 17-DEC-1998.
 XX
 PF 10-JUN-1998; 98WO-US011927.
 XX
 PR 13-JUN-1997; 97US-00874807.
 XX
 PR 14-MAY-1998; 98US-00079030.
 XX
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX
 PI Guevara JG, Hoogveen RC, Moore JP;
 XX
 DR WPI; 1999-070331/06.
 XX

PT Composition comprising nucleic acid bound to LDL or VLDL lipoprotein -
 PT used for delivering nucleic acid to cells for gene therapy and antisense
 PT treatment.
 XX
 PS Claim 19; Fig 13D; 293pp; English.

CC AAW6878-97 represent nuclear localisation signal sequence derived from
 CC human apolipoprotein B-100 (apob-100). Apob-100 is a major apoprotein
 CC component of very-low density lipoproteins (VLDL), intermediate density
 CC lipoprotein (IDL), low density lipoproteins (LDL), and lipoprotein a. The
 CC present sequence can be used in the composition of the invention. The
 CC specification describes a composition that comprises LDL and
 CC apolipoproteins for the binding and in vivo transport of nucleic acids.
 CC The composition is used to deliver nucleic acids to eukaryotic cells, in
 CC vivo or in vitro, for expressing a therapeutic polypeptide or antisense
 CC molecule (or ribozyme). Specifically they are used for gene therapy of
 CC cancers (particularly non-small cell lung carcinoma), diabetes, cystic
 CC fibrosis and arteriosclerosis
 XX
 SQ Sequence 15 AA;

Query Match
 Best Local Similarity 100.0%; Score 54; DB 2; Length 15;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TTRLTRKRGK 11
 5 TTRLTRKRGK 15

RESULT 4
 ABJ37575

ID ABJ37575 standard; peptide; 20 AA.
 XX
 AC ABJ37575;
 XX
 DT 10-MAY-2003 (first entry)
 XX
 DE Heparin binding peptide sequence #28.
 XX
 KW Cytostatic; antitumour; antidiabetic; ophthalmological;
 KW cardiovascular; circulatory; ligand; sulphated; tumour;
 KW rheumatoid arthritis; hypoxia; diabetic retinopathy; heparin.
 XX
 OS Unidentified.
 XX
 PN WO2003007689-A2.
 XX
 PD 30-JAN-2003.
 XX
 PF 22-JUL-2002; 2002MO-US023419.
 XX
 PR 20-JUL-2001; 2001US-0306726P.
 XX
 PA (ETHZ-) ETH ZUERICH.
 PA (UZYU-) UNIV ZURICH.
 PI Hubbell JA, Schoenmakers R, Maynard HD;
 DR WPI; 2003-300420/29.
 XX
 PT Use of a ligand comprising of at least one sulfated or sulfonated amino
 PT acid for the treatment of e.g. tumours, rheumatoid arthritis, diabetic
 PT retinopathy and hypoxia.
 XX
 PS Disclosure; Fig 2; 79pp; English.
 XX
 CC The invention relates to a novel ligand for binding a target biomolecule,
 CC which comprises a peptide having at least one sulphated or sulphonated
 CC amino acid and at least one amino acid chosen from neutral and positively
 CC charged amino acids. The novel ligands can be used for the treatment of
 CC e.g. tumours, rheumatoid arthritis, diabetic retinopathy and hypoxia.
 CC This sequence represents a heparin binding peptide relating to the
 CC invention
 CC
 XX
 SQ Sequence 20 AA;
 Query Match 100.0%; Score 54; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.004;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTRLTRKRGK 11
 DB 6 TTRLTRKRGK 16
 RESULT 5
 AAM57208
 ID AAM57208 standard; peptide; 22 AA.
 XX
 AC AAM57208;
 XX
 DT 03-AUG-1998 (first entry)
 XX
 DE Apo B 100 binding site peptide analogue peptide C.
 XX
 KW Apo B; binding site; receptor; cancer; drug delivery; anticancer;
 KW growth supplement; non-natural lipid particle; low density lipoprotein;
 KW LDL; receptor component; apo B100 receptor site.
 XX
 OS Synthetic.
 XX
 PN Key Location/Qualifiers
 FT Modified-site 1 /note= "attached to retinoic acid"
 FT

FT Modified-site 22
 FT /note= "attached to cholesterol"
 XX
 PN WO9813385-A2.
 XX
 PD 02-APR-1998.
 XX
 PF 25-SEP-1997; 97WO-GB002610.
 XX
 PR 27-SEP-1996; 96GB-00020153.
 XX
 PA (UYST) UNIV STRATHCLYDE.
 PI Halbert GW, Owens MD, Baillie G;
 DR WPI; 1998-230637/20.
 XX
 PT Non-natural lipid particle comprising peptide binding to apo B protein
 PT receptor - useful as, e.g. vector for delivering drugs to cancer cells
 PT that express this receptor.
 XX
 PS Claim 13; Fig 7; 73pp; English.
 XX
 CC The present sequence represents a specifically claimed Apo B 100 binding
 CC site peptide analogue which can be used as a component of a non-
 CC naturally occurring, receptor-competent low density lipoprotein (LDL)
 CC particle of the present invention. The LDL particle comprises at least 1
 CC peptide component that has at least 1 binding site for an apo B protein
 CC receptor and at least 1 lipophilic substituent. Also described in the
 CC invention are peptides containing an apo B binding sequence with at least
 CC 70% identity with sequences: KAEYKNGRHH (1) or TTRLTRKRGK (2), or their
 CC dimers. Non-naturally occurring, receptor-competent LDL particles are
 CC useful as: (i) drug-targeting vectors for delivering anticancer drugs to
 CC cancer cells that express an apo B protein receptor, and (ii) additives
 CC for cell culture media especially as growth supplements. Non-naturally
 CC occurring, receptor-competent LDL particles do not require the complete
 CC apo B sequence, which is large and tends to aggregate, to provide binding
 CC affinity to an apo B protein receptor
 CC
 XX
 SQ Sequence 22 AA;
 Query Match 100.0%; Score 54; DB 2; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.0044;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTRLTRKRGK 11
 DB 6 TTRLTRKRGK 16
 RESULT 6
 AAM57209
 ID AAM57209 standard; peptide; 22 AA.
 XX
 AC AAM57209;
 XX
 DT 03-AUG-1998 (first entry)
 XX
 DE Apo B 100 binding site peptide analogue peptide D.
 XX
 KW Apo B; binding site; receptor; cancer; drug delivery; anticancer;
 KW growth supplement; non-natural lipid particle; low density lipoprotein;
 KW LDL; receptor component; apo B100 receptor site.
 XX
 OS Synthetic.
 XX
 PN Key Location/Qualifiers
 FT Modified-site 1 /note= "attached to retinoic acid"
 FT
 XX
 PN WO9813385-A2.
 XX
 PD 02-APR-1998.

XX 25-SEP-1997; 97WO-GB002610.
 PF 27-SEP-1996; 96GB-00020153.
 PR (UYST) UNIV STRATHCLYDE.
 PA Halbert GW, Owens MD, Baillie G,
 PI WPI; 1998-230637/20.
 XX

PT Non-natural lipid particle comprising peptide binding to apo B protein
 PT receptor - useful as, e.g. vector for delivering drugs to cancer cells
 PS that express this receptor.
 XX
 PS Claim 13; Fig 7; 73pp; English.

CC The present sequence represents a specifically claimed Apo B 100 binding
 CC site peptide analogue which can be used as a component of a non-
 CC naturally occurring, receptor-competent low density lipoprotein (LDL)
 CC particle of the present invention. The LDL particle comprises at least 1
 CC peptide component that has at least 1 binding site for an apo B protein
 CC receptor and at least 1 lipophilic substituent. Also described in the
 CC invention are peptides containing an apo B binding sequence with at least
 CC 70% identity with sequences: KAEYKRNKRH (1) or TTRLTRKRGK (2) or their
 CC dimers. Non-naturally occurring, receptor-competent LDL particles are
 CC useful as: (i) drug-targeting vectors for delivering anticancer drugs to
 CC cancer cells that express an apo B protein receptor, and (ii) additives
 CC for cell culture media especially as growth supplements. Non-naturally
 CC occurring, receptor-competent LDL particles do not require the complete
 CC apo B sequence, which is large and tends to aggregate, to provide binding
 CC affinity to an apo B protein receptor
 XX
 SQ Sequence 22 AA;

Query Match Best Local Similarity 100.0%; Score 54; DB 2; Length 22;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTRLTRKRGK 11
 DB 6 TTRLTRKRGK 16

RESULT 7
 ID AAE14541 standard; peptide; 34 AA.
 XX AAE14541;
 AC 17-MAY-2002 (first entry)
 DT
 XX Human apob-100 derived peptide p62.
 DE
 XX Oxidised low density lipoprotein; oxLDL; immunoassay; pericarditis;
 KW cardiovascular disease; coronary heart disease; pre-eclampsia;
 KW non-insulin-dependent diabetes; endothelial dysfunction; human; apob-100;
 XX peptide p62.
 OS Homo sapiens.
 XX
 PN WO200206314-A2.
 XX
 PD 24-JAN-2002.
 PF 18-JUL-2001; 2001WO-GB003212.
 PR 18-JUL-2000; 2000GB-00017641.
 PA (ARKT-) ARK THERAPEUTICS LTD.
 XX Narvanen O, Yla-Herttuala S,
 PI
 XX

DR WPI; 2002-179777/23.
 XX
 PT New peptide useful in enzyme immunoassays for detecting oxidized low
 PT density lipoprotein which is a marker of coronary heart disease and other
 PT cardiovascular diseases, has affinity for oxidized low density
 PS lipoprotein.
 XX
 PS Claim 6; Page 5; 21pp; English.

CC The invention relates to peptides having affinity for oxidised low
 CC density lipoprotein (oxLDL), in cyclised or multimeric form. The peptide
 CC is useful in an immunoassay to determine the presence, and optionally,
 CC the amount of antibodies in a sample, having affinity for oxLDL.
 CC Preferably immobilised peptide is useful for measuring the amount of
 CC autoantibodies for oxLDL in a sample, especially a serum or plasma sample
 CC from a patient for evaluating the risk of coronary heart diseases, other
 CC cardiovascular diseases, and several other disorders such as
 CC pericarditis, pre-eclampsia, non-insulin-dependent diabetes and
 CC endothelial dysfunction. The peptide of the invention is stable, can be
 CC blood, and has a long half-life. The present sequence is human apob-100
 CC derived peptide p62 used in the invention
 XX
 SQ Sequence 34 AA;

Query Match Best Local Similarity 100.0%; Score 54; DB 5; Length 34;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTRLTRKRGK 11
 DB 24 TTRLTRKRGK 34

RESULT 8
 ID AAW96876 standard; peptide; 36 AA.
 XX AAW96876;
 AC 22-APR-1999 (first entry)
 DT
 XX Nucleic acid binding domain from apob-100, residues 3348-3390.
 DE
 XX Human apolipoprotein B-100; apob-100; very-low density lipoprotein; VLDL;
 KW apolipoprotein; binding; in vivo transport; nucleic acid; binding domain;
 KW nuclear localisation sequence; gene therapy; cancer; cystic fibrosis;
 XX non-small cell lung carcinoma; diabetes; arteriosclerosis.
 OS Homo sapiens.
 XX
 PN WO9856938-A1.
 XX
 PD 17-DEC-1998.
 PF 10-JUN-1998; 98WO-US011927.
 PR 13-JUN-1997; 97US-00874807.
 PR 14-MAY-1998; 98US-00079030.
 XX
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX
 PI Guevara JG, Hoogeween RC, Moore JP;
 DR WPI; 1999-070331/06.
 XX
 PT Composition comprising nucleic acid bound to LDL or VLDL lipoprotein -
 PT used for delivering nucleic acid to cells for gene therapy and antisense
 XX treatment.
 PS Claim 16; Fig 12C; 293pp; English.
 XX
 CC AAW96827-77 represent nucleic acid binding domains derived from human

OY 1 TTRLTRKRGK 11
DB 5 TTRLTRKRGK 15

RESULT 11

ABB37687
ID ABB37687 standard; peptide; 343 AA.
XX
AC ABB37687;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #5193 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.

PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000669.

XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.
XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483447/52.

XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX
PS Claim 27; SEQ ID NO 30322; 639pp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human foetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 343 AA;

Query Match 100.0%; Score 54; DB 4; Length 343;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTRLTRKRGK 11
DB 168 TTRLTRKRGK 178

RESULT 12

ABG52504
ID ABG52504 standard; peptide; 343 AA.
XX
AC ABG52504;
XX
DT 25-FEB-2003 (first entry)
XX

DE Human liver peptide, SEQ ID No 31152.
XX
XX Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX hypercholesterolaemia; coronary heart disease.
XX
OS Homo sapiens.

PN WO200157273-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000664.

XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.
XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488898/53.

XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
XX
PS Claim 27; SEQ ID NO 31152; 659pp; English.

XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABG47348-ABG59930 represent human
CC liver single exon encoded peptides of the invention. Note: The sequence
CC information for this patent does not appear in the printed specification
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 343 AA;

Query Match 100.0%; Score 54; DB 4; Length 343;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTRLTRKRGK 11
DB 168 TTRLTRKRGK 178

RESULT 13

AAR72704
ID AAR72704 standard; protein; 377 AA.
XX
AC AAR72704;
XX
DT 31-OCT-1995 (first entry)
XX
DE Human apo B-100 polypeptide 89.
XX
KW Apo B-100; hybridoma MB47; LDL cholesterol; low density lipoprotein;
XX lipid.
XX
OS Homo sapiens.

```

FH Key Location/Qualifiers
FT Peptide 1..377
FT /label= claimed
FT 140..297
FT /label= claimed
FT 173..297
FT /label= claimed
FT 205..297
FT /label= claimed
FT 216..377
FT /label= claimed
FT 216..352
FT /label= claimed
FT 216..331
FT /label= claimed
FT 216..310
FT /label= claimed
FT 216..310
FT /label= claimed
FT 217..297
FT /label= claimed
FT Peptide
FT 217..297
FT /label= claimed
XX US5408038-A.
XX 18-APR-1995.
XX 08-OCT-1992; 92US-00959946.
XX 09-OCT-1991; 91US-00774633.
XX 18-JUN-1992; 92US-00901706.
XX (SCRI ) SCRIPPS RES INST.
XX Witzum JL, Koduri KR, Young SG, Smith RS, Curtiss LK;
XX MPI, 1993-134378/16.
XX N-PSDB; AA089633.
XX Polypeptide mimic of native apo B-100 and native apo A-I - useful in
XX assays for LDL and HDL in plasma samples.
XX Claim 6; Fig 1; 41pp; English.
XX AA089633 and AA972704 depict the AA sequence of human apo B-100 and its
XX corresp. cDNA. From AA residue 3214 through residue 3590 according to the
XX numbering scheme of Ludwig et al.; DNA, 6:363 (1987). Ludwig et al.
XX reported the full cDNA sequence for the human apo B-100 gene, consisting
XX of 29 exons. AA089633 corresp. to nt 9642-10770. The apo B-100 cDNA
XX segment in AA089633 encodes an apo B-100 polypeptide called s9. Other
XX truncated AA sequences and cDNA sequences of apo B-100 identified in the
XX disclosure are: No. N terminus C terminus AA nt AA nt s1 3429 10287 3510
XX 10530 82 3418 10254 3510 10530 83 3386 10158 3510 10530 84 3353 10059
XX 3510 10530 85 3429 10287 3523 10569 86 3429 10287 3544 10632 87 3429
XX 10287 3565 10695 88 3429 10287 3590 10770 89 3214 9642 3590 10770 Forward
XX (F) and reverse (R) primers that can be used to generate a cDNA segment
XX coding for the above fragments are given in AA089633- AA089644. A
XX polypeptide is claimed which comprises an AA sequence of Apo B-100 of up
XX to 375 residues and which includes residues 217-297 and which
XX immunoreacts with antibodies generated by the hybridoma MB47 having ATCC
XX Accession No. HB 8746. Claimed polypeptides are listed in FT. A fusion
XX polypeptide is also claimed which comprises a sequence of apo A-I (see
XX AA089644/R72705) and a sequence of apo B-100
XX
SQ Sequence 377 AA;
Query Match 100.0%; Score 54; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTTLTRKRGK 11
DB 144 TTTLTRKRGK 154

```

```

RESULT 14
AA034031
ID AA034031 standard; protein; 377 AA.
XX
XX AA034031;
AC
XX
XX 25-MAR-2003 (revised)
DT 13-AUG-1993 (first entry)
XX
XX Sequence of apo B-100.
DE
XX Lipoprotein; apoprotein; B-100; A-I; LDL; HDL; assay.
XX
XX Homo sapiens.
XX
XX WO9307165-A1.
XX
XX 15-APR-1993.
XX
XX 09-OCT-1992; 92WO-US008634.
XX
XX 09-OCT-1991; 91US-00774633.
XX 18-JUN-1992; 92US-00901706.
XX 08-OCT-1992; 92US-00959946.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Smith RS, Curtiss LK, Koduri KR, Witzum JL, Young SG;
XX MPI, 1993-134378/16.
XX N-PSDB; AA040029.
XX
XX Polypeptide mimic of native apo B-100 and native apo A-I - useful in
XX assays for LDL and HDL in plasma samples.
XX Claim 6; Page 103-104; 137pp; English.
XX
XX The inventors claim a portion of the polypeptide contg. apo B-100 that
XX immunoreacts with antibodies secreted by the hybridoma MB47 having ATCC
XX Accession No. 8746. Polypeptides specifically claimed include residues
XX 217-297, 216-310, 216-331, 216-352, 216-377, 1-377, 205-297, 173-297, 140
XX -297. DNA sequences encoding the polypeptides are also claimed. Also
XX claimed are a fusion polypeptide that contains: (a) a first amino
XX acid residue sequence up to 250 residues in length that includes residues
XX 120-135 of apo A-I, (b) a second amino acid residue sequence up to 375
XX residues in length that includes residues 217-297 of apo B-100 and DNA
XX encoding it. (Updated on 25-MAR-2003 to correct pn field.) (Updated on 25
XX -MAR-2003 to correct pr field.)
XX
SQ Sequence 377 AA;
Query Match 100.0%; Score 54; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTTLTRKRGK 11
DB 144 TTTLTRKRGK 154

```

RESULT 15

```

ADJ57400
ID ADJ57400 standard; protein; 2463 AA.
XX
XX ADJ57400;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Human apolipoprotein B, marker for hepatocellular carcinoma.
XX
XX Hepatocellular carcinoma; marker; human; apolipoprotein B; diagnosis.
XX

```

OS Homo sapiens.
 XX
 PN WO2004005466-A2.
 XX
 PD 15-JAN-2004.
 XX
 PF 03-JUL-2003; 2003WO-US020841.
 XX
 PR 03-JUL-2002; 2002US-0393982P.
 XX
 PA (ILLU-) ILLUMIGEN BIOSCIENCES INC.
 XX
 PI Katze M, Bumgarner R, Smit M, Rosenberg G;
 XX
 DR WPI; 2004-142977/14.
 DR GENBANK; NP_000375.
 XX
 PT Detecting hepatocellular carcinoma (HCC) in mammals comprises obtaining
 PT and assaying a biological sample to quantify a cell-associated or a non-
 PT cell-associated HCC-related protein and comparing the quantity to a
 PT control level.
 XX
 PS Disclosure; SEQ ID NO 4; 48bp; English.
 XX
 CC The present sequence is that of human apolipoprotein B. This non-cell
 CC associated protein is one of a set of proteins characterised as
 CC diagnostic targets for hepatocellular carcinoma (HCC). Such proteins are
 CC the products of genes identified by expression microarray analysis of
 CC tumour samples from hepatitis C virus (HCV) infected patients with HCC as
 CC being specifically up-regulated in HCC tumour tissue when compared to HCV
 CC infected cirrhotic non-tumour tissue and normal liver. The invention
 CC relates to the detection of HCC by assaying patient samples such as
 CC tissue, plasma, serum, etc. for the presence and level of specific HCC
 CC related proteins. A finding of elevated levels of one or more of these
 CC proteins in a patient sample indicates that the patient has HCC. Methods
 CC for the diagnosis of HCC are provided, as well as improved assay methods
 CC and scanning methods that employ non-cell-associated and cell-associated
 CC HCC-related proteins.
 CC
 SQ Sequence 2463 AA;
 SQ
 Query Match 100.0%; Score 54; DB 8; Length 2463;
 Best Local Similarity 100.0%; Pred. No. 0.45;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTRLTRRGGK 11
 |||||
 Db 1284 TTRLTRRGGK 1294

Search completed: January 12, 2005, 13:25:40
 Job time : 102.484 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2005, 13:14:21 ; Search time 25.9032 Seconds
(without alignments)
28.162 Million cell updates/sec

Title: US-10-657-404a-2
Perfect score: 54
Sequence: 1 TTRLTRKRGK 11

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/1/aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/1/aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/aa/PCtUS.COMB.pep: *
6: /cgn2_6/ptodata/1/aa/backfilest.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	11	4	US-09-269-533A-2
2	54	100.0	13	4	US-09-269-533A-4
3	54	100.0	15	4	US-09-079-030-205
4	54	100.0	22	4	US-09-269-533A-5
5	54	100.0	22	4	US-09-269-533A-6
6	54	100.0	36	4	US-09-079-030-166
7	54	100.0	51	4	US-09-079-030-98
8	54	100.0	377	1	US-07-959-946-1
9	54	100.0	377	1	US-08-333-577-1
10	54	100.0	377	5	PCT-US92-08634-1
11	54	100.0	420	4	US-09-079-030-223
12	54	100.0	840	4	US-09-079-030-214
13	54	100.0	4536	4	US-09-180-422B-27
14	54	100.0	4536	4	US-09-079-030-1
15	54	100.0	4563	4	US-09-108-006C-1
16	54	100.0	4563	4	US-09-538-092-842
17	50	92.6	773	4	US-09-079-030-215
18	49	90.7	15	4	US-09-265-222-20
19	49	90.7	15	4	US-09-180-422B-17
20	45	83.3	10	4	US-09-265-222-1
21	45	83.3	10	4	US-09-265-222-6
22	44	81.5	10	4	US-09-265-222-5
23	44	81.5	10	4	US-09-265-222-7
24	44	81.5	10	4	US-09-265-222-9
25	44	81.5	10	4	US-09-265-222-11
26	44	81.5	11	4	US-09-269-533A-3
27	44	81.5	12	4	US-09-180-422B-13

28	44	81.5	15	3	US-08-981-122-85	Sequence 85, Appl
29	44	81.5	785	4	US-09-079-030-216	Sequence 216, App
30	43	79.6	10	4	US-09-265-222-2	Sequence 2, Appl1
31	43	79.6	10	4	US-09-265-222-3	Sequence 3, Appl1
32	43	79.6	10	4	US-09-265-222-4	Sequence 4, Appl1
33	42	77.8	10	4	US-09-265-222-8	Sequence 8, Appl1
34	42	77.8	10	4	US-09-265-222-10	Sequence 10, Appl
35	42	77.8	10	4	US-09-265-222-12	Sequence 12, Appl
36	40	74.1	336	4	US-09-489-039A-13630	Sequence 13630, A
37	38.5	71.3	11	4	US-09-265-222-16	Sequence 16, Appl
38	38.5	71.3	11	4	US-09-265-222-17	Sequence 17, Appl
39	38.5	71.3	11	4	US-09-265-222-18	Sequence 18, Appl
40	38.5	71.3	11	4	US-09-265-222-19	Sequence 19, Appl
41	36	66.7	316	4	US-09-543-681A-4590	Sequence 4590, Ap
42	35	64.8	124	4	US-09-732-210-593	Sequence 693, App
43	35	64.8	390	3	US-09-108-020-36	Sequence 36, Appl
44	35	64.8	390	4	US-09-901-151-5	Sequence 5, Appl1
45	35	64.8	390	4	US-09-901-151-6	Sequence 6, Appl1

ALIGNMENTS

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RESULT 1
US-09-269-533A-2
; Sequence 2, Application US/09269533A
; Patent No. 6670452
; GENERAL INFORMATION:
; APPLICANT: University of Strathclyde
; APPLICANT: Halbert, Gavin
; APPLICANT: Owens, Moira
; APPLICANT: Bailie, George
; TITLE OF INVENTION: No. 6670452-Naturally Occurring Lipoprotein Particle
; FILE REFERENCE: P07885US
; CURRENT APPLICATION NUMBER: US/09/269,533A
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: PCT/GB97/02610
; PRIOR FILING DATE: 1997-09-25
; PRIOR APPLICATION NUMBER: GB 9620153.8
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..1)
; OTHER INFORMATION: Apo B binding site sequence
US-09-269-533A-2
Query Match 100.0%; Score 54; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 TTRLTRKRGK 11
Db 1 TTRLTRKRGK 11
RESULT 2
US-09-269-533A-4
; Sequence 4, Application US/09269533A
; Patent No. 6670452
; GENERAL INFORMATION:
; APPLICANT: University of Strathclyde
; APPLICANT: Halbert, Gavin
; APPLICANT: Owens, Moira
; APPLICANT: Bailie, George
; TITLE OF INVENTION: No. 6670452-Naturally Occurring Lipoprotein Particle
; FILE REFERENCE: P07885US
; CURRENT APPLICATION NUMBER: US/09/269,533A
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/ CURRENT FILING DATE: 1999-06-01
/ PRIOR APPLICATION NUMBER: PCT/GB97/02610
/ PRIOR FILING DATE: 1997-09-25
/ PRIOR APPLICATION NUMBER: GB 9620153.8
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 4
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: (1..7)
/ OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site
/ NAME/KEY: misc.feature
/ LOCATION: (1..7)
/ OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue
US-09-269-533A-4
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Query Match

Best Local Similarity 100.0%; Score 54; DB 4; Length 13;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTRLTRRRGK 11
Db 2 TTRLTRRRGK 12

RESULT 3

US-09-079-030-205

/ Sequence 205, Application US/09079030
/ Patent No. 6635623

/ GENERAL INFORMATION:

/ APPLICANT: Guevera, Jr., Juan G.

/ APPLICANT: Hoogeveen, Ron C.

/ APPLICANT: Moore, Paul J.

/ TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY

/ NUMBER OF SEQUENCES: 229
/ VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS

/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Arnold, White & Durkee

/ STREET: P.O. Box 4433

/ CITY: Houston

/ STATE: Texas

/ COUNTRY: USA

/ ZIP: 77210

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: PatentIn Release #1.0, Version #1.30

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/079,030

/ FILING DATE: Concurrently Herewith

/ CLASSIFICATION:

/ ATTORNEY/AGENT INFORMATION:

/ NAME: McMillian, Nabeela R.

/ REGISTRATION NUMBER: P-43,363

/ REFERENCE/DOCKET NUMBER: ARAG:003

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 512/418-3000

/ TELEFAX: 512/474-7577

/ INFORMATION FOR SEQ ID NO: 205:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 15 amino acids

/ TYPE: amino acid

/ STRANDEDNESS:

/ TOPOLOGY: linear

Query Match

Best Local Similarity 100.0%; Score 54; DB 4; Length 15;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTRLTRRRGK 11
Db 2 TTRLTRRRGK 12

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTRLTRRRGK 11
Db 5 TTRLTRRRGK 15

RESULT 4

US-09-269-533A-5

/ Sequence 5, Application US/09269533A
/ Patent No. 6670452

/ GENERAL INFORMATION:

/ APPLICANT: University of Strathclyde

/ APPLICANT: Halbert, Gavin

/ APPLICANT: Owens, Moira

/ APPLICANT: Baillie, George

/ TITLE OF INVENTION: No. 6670452-Naturally Occurring Lipoprotein Particle

/ FILE REFERENCE: P0788505

/ CURRENT APPLICATION NUMBER: US/09/269,533A

/ PRIOR FILING DATE: 1999-06-01

/ PRIOR APPLICATION NUMBER: PCT/GB97/02610

/ PRIOR FILING DATE: 1997-09-25

/ PRIOR APPLICATION NUMBER: GB 9620153.8

/ NUMBER OF SEQ ID NOS: 7

/ SOFTWARE: PatentIn version 3.0

/ SEQ ID NO 5

/ LENGTH: 22

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE:

/ NAME/KEY: misc.feature

/ LOCATION: (1..7)

/ OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site

/ NAME/KEY: misc.feature

/ LOCATION: (1..7)

/ OTHER INFORMATION: Cholesterol linked at C-terminus of peptide analogue

/ NAME/KEY: misc.feature

/ LOCATION: (1..7)

/ OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue

/ US-09-269-533A-5

/ Sequence 6, Application US/09269533A

/ Patent No. 6670452

/ GENERAL INFORMATION:

/ APPLICANT: University of Strathclyde

/ APPLICANT: Halbert, Gavin

/ APPLICANT: Owens, Moira

/ APPLICANT: Baillie, George

/ TITLE OF INVENTION: No. 6670452-Naturally Occurring Lipoprotein Particle

/ FILE REFERENCE: P0788505

/ CURRENT APPLICATION NUMBER: US/09/269,533A

/ PRIOR FILING DATE: 1999-06-01

/ PRIOR APPLICATION NUMBER: PCT/GB97/02610

/ PRIOR FILING DATE: 1997-09-25

/ PRIOR APPLICATION NUMBER: GB 9620153.8

/ NUMBER OF SEQ ID NOS: 7

/ SOFTWARE: PatentIn version 3.0

/ SEQ ID NO 6

/ LENGTH: 22

/ TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc feature
LOCATION: (1..7)
OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site
NAME/KEY: misc feature
LOCATION: (1..7)
OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue
US-09-269-533A-6

Query Match 100.0%; Score 54; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.00095;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11
|||
Db 6 TTRLTRKRGK 16

RESULT 6
US-09-079-030-166
Sequence 166, Application US/09079030
Patent No. 6635623
GENERAL INFORMATION:
APPLICANT: Guevera, Jr., Juan G.
APPLICANT: Hoogeveen, Ron C.
APPLICANT: Moore, Paul J.
TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
TITLE OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
NUMBER OF SEQUENCES: 229
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,030
FILING DATE: Concurrently Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMillian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: ARAG:003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 166:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-079-030-166

Query Match 100.0%; Score 54; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11
|||
Db 10 TTRLTRKRGK 20

RESULT 7
US-09-079-030-98
Sequence 98, Application US/09079030

Patent No. 6635623
GENERAL INFORMATION:
APPLICANT: Guevera, Jr., Juan G.
APPLICANT: Hoogeveen, Ron C.
APPLICANT: Moore, Paul J.
TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
TITLE OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
NUMBER OF SEQUENCES: 229
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,030
FILING DATE: Concurrently Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMillian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: ARAG:003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-079-030-98

Query Match 100.0%; Score 54; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11
|||
Db 5 TTRLTRKRGK 15

RESULT 8
US-07-959-946-1
Sequence 1, Application US/07959946
Patent No. 5408038
GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Witzum, Joseph L.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dresler, Goldsmith, Shore, Sucker &
ADDRESSEE: Malinow, Ltd.
STREET: 180 No. 5408038th Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: US/07/959,946
 CLASSIFICATION: 19921008
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 435
 FILING DATE: 18-JUN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Gamsen, Edward P.
 REGISTRATION NUMBER: 29,381
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312)616-5400
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 377 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-959-946-1

Query Match
 Best Local Similarity 100.0%; Score 54; DB 1; Length 377;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTRLTRKRGK 11
 DB 144 TTRLTRKRGK 154

RESULT 9
 US-08-333-577-1
 Sequence 1, Application US/08333577
 Patent No. 5786206
 GENERAL INFORMATION:
 APPLICANT: Smith, Richard K.
 APPLICANT: Koduri, Raju
 APPLICANT: Young, Stephen G.
 APPLICANT: Witzum, Joseph L.
 APPLICANT: Curtiss, Linda K.
 TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Dressler, Goldsmith, Shore, Suter &
 STREET: 180 No. 5786206th Stetson, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/333,577
 FILING DATE:
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Gamsen, Edward P.
 REGISTRATION NUMBER: 29,381
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312)616-5400
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 377 amino acids
 TYPE: amino acid

TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-333-577-1
 Query Match
 Best Local Similarity 100.0%; Score 54; DB 1; Length 377;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTRLTRKRGK 11
 DB 144 TTRLTRKRGK 154

RESULT 10
 PCT-US92-08634-1
 Sequence 1, Application PC/TUS9208634
 GENERAL INFORMATION:
 APPLICANT: Smith, Richard K.
 APPLICANT: Koduri, Raju
 APPLICANT: Young, Stephen G.
 APPLICANT: Witzum, Joseph L.
 APPLICANT: Curtiss, Linda K.
 TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Dressler, Goldsmith, Shore, Suter &
 STREET: 180 North Stetson, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/08634
 FILING DATE: 19921009
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,706
 FILING DATE: 18-JUN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Gamsen, Edward P.
 REGISTRATION NUMBER: 29,381
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312)616-5400
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 377 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US92-08634-1

Query Match
 Best Local Similarity 100.0%; Score 54; DB 5; Length 377;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTRLTRKRGK 11
 DB 144 TTRLTRKRGK 154

RESULT 11
 US-09-079-030-223
 Sequence 223, Application US/09079030
 Patent No. 6635623

GENERAL INFORMATION:
APPLICANT: Guevera, Jr., Juan G.
APPLICANT: Hoogveen, Ron C.
TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
TITLE OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
NUMBER OF SEQUENCES: 229
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,030
FILING DATE: Concurrently Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMillian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: ARAG:003
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 223:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-079-030-223

Query Match 100.0%; Score 54; DB 4; Length 420;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11
Db 57 TTRLTRKRGK 67

RESULT 12
US-09-079-030-214
Sequence 214 Application US/09079030
Patent No. 6635623
GENERAL INFORMATION:
APPLICANT: Guevera, Jr., Juan G.
APPLICANT: Hoogveen, Ron C.
APPLICANT: Moore, Paul J.
TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
TITLE OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
NUMBER OF SEQUENCES: 229
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,030
FILING DATE: Concurrently Herewith

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMillian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: ARAG:003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-079-030-214

Query Match 100.0%; Score 54; DB 4; Length 840;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11
Db 657 TTRLTRKRGK 667

RESULT 13
US-09-180-422B-27
Sequence 27 Application US/09180422B
Patent No. 6444644
GENERAL INFORMATION:
APPLICANT: BRUCKDORFER, KARL R
TITLE OF INVENTION: ANTICOAGULANT PEPTIDE FRAGMENTS DERIVED
FROM APOLIPOPROTEIN B-100
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE, P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/180,422B
FILING DATE: 07-Dec-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36663
REFERENCE/DOCKET NUMBER: 117-268
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 4536 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-180-422B-27

Query Match 100.0%; Score 54; DB 4; Length 4536;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11

Db 3357 TTRLTRKRGK 3367

RESULT 14

US-09-079-030-1
Sequence 1, Application US/09079030
Patent No. 6635623

GENERAL INFORMATION:

APPLICANT: Guevera, Jr., Juan G.
APPLICANT: Hoogveen, Ron C.

APPLICANT: Moore, Paul J.

TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY

NUMBER OF SEQUENCES: 229
VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/079,030

FILING DATE: Concurrently Herewith

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: McWilliam, Nabeela R.

REGISTRATION NUMBER: P-43,363

REFERENCE/DOCKET NUMBER: ARAG-003

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4536 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-09-079-030-1

Query Match 100.0%; Score 54; DB 4; Length 4536;

Best Local Similarity 100.0%; Pred. No. 0.2; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTRLTRKRGK 11

Db 3357 TTRLTRKRGK 3367

RESULT 15

US-09-108-006C-1
Sequence 1, Application US/09108006C
Patent No. 6524613

GENERAL INFORMATION:

APPLICANT: Steer, Clifford J.
Kren, Betsy T.

Bandyopadhyay, Paramita

Roy-Chowdhury, Jayanta

TITLE OF INVENTION: Hepatocellular Chimera

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kimeragen, Inc.

STREET: 300 Pleasant Run

CITY: Newtown

STATE: PA

COUNTRY: USA

ZIP: 18940

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/108,006C

FILING DATE: 30-Jun-1992

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/054,288

FILING DATE: 30-APR-1997

APPLICATION NUMBER: 60/054,837

FILING DATE: 05-AUG-1997

APPLICATION NUMBER: 60/064,996

FILING DATE: 10-NOV-1997

APPLICATION NUMBER: 60/074,497

FILING DATE: 12-FEB-1998

APPLICATION NUMBER: PCT US 98/08834

FILING DATE: 30-APR-1998

ATTORNEY/AGENT INFORMATION:

NAME: Fiebel, Thomas

REGISTRATION NUMBER: 29258

REFERENCE/DOCKET NUMBER: 7991-015-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-504-4444

TELEFAX: 215-504-4545

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4563 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-108-006C-1

Query Match 100.0%; Score 54; DB 4; Length 4563;

Best Local Similarity 100.0%; Pred. No. 0.2; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTRLTRKRGK 11

Db 3384 TTRLTRKRGK 3394

Search completed: January 12, 2005, 13:33:16
Job time : 26.9032 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: January 12, 2005, 13:31:02 ; Search time 88.3548 Seconds
(without alignments)
44.980 Million cell updates/sec

Title: US-10-657-404A-2
Perfect score: 54
Sequence: 1 TTRLTRKRGK 11

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues
Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	54	100.0	11	9	US-09-269-533A-2
2	54	100.0	11	17	US-10-657-404A-2
3	54	100.0	13	9	US-09-269-533A-4
4	54	100.0	13	17	US-10-657-404A-4
5	54	100.0	22	9	US-09-269-533A-5
6	54	100.0	22	9	US-09-269-533A-6
7	54	100.0	22	17	US-10-657-404A-5
8	54	100.0	22	17	US-10-657-404A-6
9	54	100.0	25	17	US-10-657-404A-9
10	54	100.0	34	15	US-10-333-313-1
11	54	100.0	343	9	US-09-864-761-46837
12	54	100.0	3000	16	US-10-741-601-431
13	54	100.0	4563	9	US-09-870-759-128

14	54	100.0	4563	10	US-09-802-640-32	Sequence 37, Appl
15	54	100.0	4563	10	US-09-751-708A-128	Sequence 128, App
16	54	100.0	4563	14	US-10-403-902A-32	Sequence 32, Appl
17	54	100.0	4563	16	US-10-741-601-432	Sequence 432, App
18	54	100.0	4563	16	US-10-741-601-433	Sequence 433, App
19	54	100.0	4563	17	US-10-428-817A-124	Sequence 124, App
20	49	90.7	10	9	US-09-823-418-20	Sequence 20, Appl
21	49	90.7	10	9	US-09-822-965-20	Sequence 20, Appl
22	45	83.3	10	9	US-09-823-418-1	Sequence 1, Appl
23	45	83.3	10	9	US-09-823-418-6	Sequence 6, Appl
24	45	83.3	10	9	US-09-822-965-1	Sequence 1, Appl
25	45	83.3	10	9	US-09-822-965-6	Sequence 6, Appl
26	45	83.3	10	10	US-09-572-404B-595	Sequence 595, App
27	45	83.3	10	10	US-09-572-404B-635	Sequence 635, App
28	45	83.3	10	10	US-09-572-404B-729	Sequence 729, App
29	44	81.5	9	17	US-10-657-404A-8	Sequence 8, Appl
30	44	81.5	10	9	US-09-823-418-5	Sequence 5, Appl
31	44	81.5	10	9	US-09-823-418-7	Sequence 7, Appl
32	44	81.5	10	9	US-09-823-418-9	Sequence 9, Appl
33	44	81.5	10	9	US-09-823-418-11	Sequence 11, Appl
34	44	81.5	10	9	US-09-822-965-5	Sequence 5, Appl
35	44	81.5	10	9	US-09-822-965-7	Sequence 7, Appl
36	44	81.5	10	9	US-09-822-965-9	Sequence 9, Appl
37	44	81.5	10	9	US-09-822-965-11	Sequence 11, Appl
38	44	81.5	11	9	US-09-269-533A-3	Sequence 3, Appl
39	44	81.5	11	9	US-09-398-902-2	Sequence 2, Appl
40	44	81.5	11	10	US-09-931-375A-76	Sequence 76, Appl
41	44	81.5	11	14	US-10-358-594-2	Sequence 2, Appl
42	44	81.5	11	17	US-10-657-404A-3	Sequence 3, Appl
43	44	79.6	10	9	US-09-823-418-2	Sequence 2, Appl
44	44	79.6	10	9	US-09-823-418-3	Sequence 3, Appl
45	43	79.6	10	9	US-09-823-418-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-269-533A-2
; Sequence 2, Application US/09269533A
; Patent No. US20020147304A1
; GENERAL INFORMATION:
; APPLICANT: University of Strathclyde
; APPLICANT: Halbert, Gavin
; APPLICANT: Owens, Moira
; APPLICANT: Baillie, George
; TITLE OF INVENTION: No. US20020147304A1-Naturally Occurring Lipoprotein Particle
; FILE REFERENCE: P07885US
; CURRENT APPLICATION NUMBER: US-09/269, 533A
; CURRENT FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: PCT/GB97/02610
; PRIOR FILING DATE: 1997-09-25
; PRIOR APPLICATION NUMBER: GB 9620153.8
; PRIOR FILING DATE: 1996-09-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..7)
; OTHER INFORMATION: Apo B binding site sequence
US-09-269-533A-2
Query Match 100.0%; Score 54; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 TTRLTRKRGK 11
Db 1 TTRLTRKRGK 11

RESULT 2

US-10-657-404A-2
; Sequence 2, Application US/10657404A
; Publication No. US20040235730A1
; GENERAL INFORMATION:
; APPLICANT: University of Strathclyde
; APPLICANT: Halbert, Gavin
; APPLICANT: Owens, Moira
; APPLICANT: Baillie, George
; TITLE OF INVENTION: Non-Naturally Occurring Lipoprotein Particle
; FILE REFERENCE: P07885US-CIP
; CURRENT APPLICATION NUMBER: US/10/657,404A
; PRIOR FILING DATE: 1997-09-25
; PRIOR APPLICATION NUMBER: PCT/GB97/02610
; PRIOR FILING DATE: 1997-09-25
; PRIOR APPLICATION NUMBER: GB 9620153.8
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Apo B binding site sequence
US-10-657-404A-2

Query Match

Best Local Similarity 100.0%; Score 54; DB 17; Length 11;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLTRRGK 11
Db 1 TTRLTRRGK 11

RESULT 3

US-09-269-533A-4
; Sequence 4, Application US/09269533A
; Patent No. US20020147304A1
; GENERAL INFORMATION:
; APPLICANT: University of Strathclyde
; APPLICANT: Halbert, Gavin
; APPLICANT: Owens, Moira
; APPLICANT: Baillie, George
; TITLE OF INVENTION: No. US20020147304A1-Naturally Occurring Lipoprotein Particle
; FILE REFERENCE: P07885US
; CURRENT APPLICATION NUMBER: US/09/269,533A
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: PCT/GB97/02610
; PRIOR FILING DATE: 1997-09-25
; PRIOR APPLICATION NUMBER: GB 9620153.8
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (..T)
; OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site
; LOCATION: (..T)
; OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue
US-09-269-533A-4

Query Match

Best Local Similarity 100.0%; Score 54; DB 9; Length 13;
Matches 100.0%; Pred. No. 0.0038;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLTRRGK 11
Db 2 TTRLTRRGK 12

RESULT 4

US-10-657-404A-4
; Sequence 4, Application US/10657404A
; Publication No. US20040235730A1
; GENERAL INFORMATION:
; APPLICANT: University of Strathclyde
; APPLICANT: Halbert, Gavin
; APPLICANT: Owens, Moira
; APPLICANT: Baillie, George
; TITLE OF INVENTION: Non-Naturally Occurring Lipoprotein Particle
; FILE REFERENCE: P07885US-CIP
; CURRENT APPLICATION NUMBER: US/10/657,404A
; PRIOR FILING DATE: 1997-09-25
; PRIOR APPLICATION NUMBER: PCT/GB97/02610
; PRIOR FILING DATE: 1997-09-25
; PRIOR APPLICATION NUMBER: GB 9620153.8
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site
; NAME/KEY: misc feature
; OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue
US-10-657-404A-4

Query Match

Best Local Similarity 100.0%; Score 54; DB 17; Length 13;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLTRRGK 11
Db 2 TTRLTRRGK 12

RESULT 5

US-09-269-533A-5
; Sequence 5, Application US/09269533A
; Patent No. US20020147304A1
; GENERAL INFORMATION:
; APPLICANT: University of Strathclyde
; APPLICANT: Halbert, Gavin
; APPLICANT: Owens, Moira
; APPLICANT: Baillie, George
; TITLE OF INVENTION: No. US20020147304A1-Naturally Occurring Lipoprotein Particle
; FILE REFERENCE: P07885US
; CURRENT APPLICATION NUMBER: US/09/269,533A
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: PCT/GB97/02610
; PRIOR FILING DATE: 1997-09-25
; PRIOR APPLICATION NUMBER: GB 9620153.8
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (..T)

Query Match

Best Local Similarity 100.0%; Score 54; DB 9; Length 13;
Matches 100.0%; Pred. No. 0.0038;

OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site
NAME/KEY: misc feature
LOCATION: (1..1)
OTHER INFORMATION: Cholesterol linked at C-terminus of peptide analogue
NAME/KEY: misc feature
LOCATION: (1..1)
OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue
US-09-269-533A-5

Query Match 100.0%; Score 54; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11
Db 6 TTRLTRKRGK 16

RESULT 6

US-09-269-533A-6
Sequence 6, Application US/09269533A
Patent No. US20020147304A1
GENERAL INFORMATION:
APPLICANT: University of Strathclyde
APPLICANT: Halbert, Gavin
APPLICANT: Owens, Moira
APPLICANT: Baillie, George
TITLE OF INVENTION: No. US20020147304A1-Naturally Occurring Lipoprotein Particle
FILE REFERENCE: P07885US
CURRENT APPLICATION NUMBER: US/09/269, 533A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: PCT/GB97/02610
PRIOR FILING DATE: 1997-09-25
PRIOR APPLICATION NUMBER: GB 9620153.8
PRIOR FILING DATE: 1996-09-27
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 22
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc feature
LOCATION: (1..1)
OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site
NAME/KEY: misc feature
LOCATION: (1..1)
OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue
US-09-269-533A-6

Query Match 100.0%; Score 54; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11
Db 6 TTRLTRKRGK 16

RESULT 7

US-10-657-404A-5
Sequence 5, Application US/10657404A
Publication No. US20040235730A1
GENERAL INFORMATION:
APPLICANT: University of Strathclyde
APPLICANT: Halbert, Gavin
APPLICANT: Owens, Moira
APPLICANT: Baillie, George
TITLE OF INVENTION: Non-Naturally Occurring Lipoprotein Particle
FILE REFERENCE: P07885US-CIP
CURRENT APPLICATION NUMBER: US/10/657, 404A
CURRENT FILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: PCT/GB97/02610

PRIOR FILING DATE: 1997-09-25
PRIOR APPLICATION NUMBER: GB 9620153.8
PRIOR FILING DATE: 1996-09-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 22
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site
NAME/KEY: misc feature
LOCATION: (1..1)
OTHER INFORMATION: Cholesterol linked at C-terminus of peptide analogue
NAME/KEY: misc feature
LOCATION: (1..1)
OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue
US-10-657-404A-5

Query Match 100.0%; Score 54; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11
Db 6 TTRLTRKRGK 16

RESULT 8

US-10-657-404A-6
Sequence 6, Application US/10657404A
Publication No. US20040235730A1
GENERAL INFORMATION:
APPLICANT: University of Strathclyde
APPLICANT: Halbert, Gavin
APPLICANT: Owens, Moira
APPLICANT: Baillie, George
TITLE OF INVENTION: Non-Naturally Occurring Lipoprotein Particle
FILE REFERENCE: P07885US-CIP
CURRENT APPLICATION NUMBER: US/10/657, 404A
CURRENT FILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: PCT/GB97/02610
PRIOR FILING DATE: 1997-09-25
PRIOR APPLICATION NUMBER: GB 9620153.8
PRIOR FILING DATE: 1996-09-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 22
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site
NAME/KEY: misc feature
LOCATION: (1..1)
OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue
US-10-657-404A-6

Query Match 100.0%; Score 54; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11
Db 6 TTRLTRKRGK 16

RESULT 9

US-10-657-404A-9
Sequence 9, Application US/10657404A
Publication No. US20040235730A1

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/ GENERAL INFORMATION:
/ APPLICANT: University of Strathclyde
/ APPLICANT: Halder, Gavin
/ APPLICANT: Owens, Moira
/ APPLICANT: Baillie, George
/ TITLE OF INVENTION: Non-Naturally Occurring Lipoprotein Particle
/ FILE REFERENCE: P0785US-CIP
/ CURRENT APPLICATION NUMBER: US/10/657,404A
/ PRIOR FILING DATE: 2003-09-08
/ PRIOR APPLICATION NUMBER: PCT/GB97/02610
/ PRIOR FILING DATE: 1997-09-25
/ PRIOR APPLICATION NUMBER: GB 9620153.8
/ PRIOR FILING DATE: 1996-09-27
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 9
/ LENGTH: 25
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site
/ NAME/KEY: MISC FEATURE
/ OTHER INFORMATION: Cholesterol linked at C-terminus of peptide analogue
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ OTHER INFORMATION: Pyrene butyric acid linked at N-terminus of peptide analogue
US-10-657-404a-9
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Query Match
Best Local Similarity 100.0%; Score 54; DB 17; Length 25;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 TTRLTRKRGK 11
DB 5 TTRLTRKRGK 15
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RESULT 10
US-10-333-313-1
/ Sequence 1, Application US/10333313
/ Publication No. US20040091934A1
/ GENERAL INFORMATION:
/ APPLICANT: Narvaen, Outi
/ APPLICANT: Yla-Herttuala, Seppo
/ TITLE OF INVENTION: Peptides and Their Use in Assays for Cardiovascular Disease
/ FILE REFERENCE: GJE-6363
/ CURRENT APPLICATION NUMBER: US/10/333,313
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: PCT/GB01/03212
/ PRIOR FILING DATE: 2001-07-18
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 34
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: oligopeptide
US-10-333-313-1
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Query Match
Best Local Similarity 100.0%; Score 54; DB 15; Length 34;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 TTRLTRKRGK 11
DB 24 TTRLTRKRGK 34
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RESULT 11
US-09-864-761-46837
/ Sequence 46837, Application US/09864761
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/ Patent No. US20020048763A1
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rank, David R.
/ APPLICANT: Hanzel, David K.
/ APPLICANT: Chen, Wensheng
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
/ FILE REFERENCE: Aeomica-X-1
/ CURRENT APPLICATION NUMBER: US/09/864,761
/ PRIOR FILING DATE: 2001-05-23
/ PRIOR APPLICATION NUMBER: US 60/180,312
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US 09/632,366
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 09/608,408
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/774,203
/ PRIOR FILING DATE: 2001-01-29
/ NUMBER OF SEQ ID NOS: 49117
/ SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
/ SEQ ID NO 46837
/ LENGTH: 343
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO AC010872.3
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.7
/ OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 26
/ OTHER INFORMATION: EST HUMAN HIT: A1174984.1, EVALU2 2.00e-60
/ OTHER INFORMATION: SWISSPROT HIT: P04114, EVALU2 0.00e+00
US-09-864-761-46837
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Query Match
Best Local Similarity 100.0%; Score 54; DB 9; Length 343;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 TTRLTRKRGK 11
DB 168 TTRLTRKRGK 178
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RESULT 12
US-10-741-601-431
/ Sequence 431, Application US/10741601
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; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 431
; LENGTH: 3000
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-741-601-431

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Best Local Similarity	100.0%	Pred. NO	0.88	
Matches 11, Conservative	0	Mismatches	0	Indels 0 Gaps 0

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QY      1 TTRLTRKGLK 11
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Db      2336 TTRLTRKGLK 2346
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RESULT 13
US-09-870-759-128
; Sequence 128, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIORITY APPLICATION NUMBER: US 60/208,128
; PRIORITY FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 128
; LENGTH: 4563
; TYPE: prt
; ORGANISM: Homo sapiens
; US-09-870-759-128

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Query Match	100.0%	Score 54	DB 9	Length 4563
Best Local Similarity	100.0%	Pred. No. 1.3		
Matches 11, Conservative	0	Mismatches	0	Gaps 0

Qy	1	TTRLTRKGLK	11
Db	3384	TTRLTRKGLK	3394

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1 RESULT 14
2 US-09-802-640-32
3 ; Sequence 32, Application US/09802640
4 ; Publication No. US20030036057A1
5 ; GENERAL INFORMATION:
6 ; APPLICANT: Braun, Andreas
7 ; APPLICANT: Bonnal Aruna
8 ; APPLICANT: Kleyn Patrick
9 ; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
10 ; TITLE OF INVENTION: CARCINOASCULAR DISEASE AND THEIR USE
11 ; FILE REFERENCE: 24736-2048
12 ; CURRENT APPLICATION NUMBER: US/09/802,640
13 ; CURRENT FILING DATE: 2001-03-09
14 ; NUMBER OF SEQ ID NOS: 122
15 ; SOFTWARE: FastSeq for Windows Version 4.0
16 ; SEQ ID NO 32
17 ; LENGTH: 4563
18 ; TYPE: FRT
19 ; ORGANISM: Homo sapien

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US-09-802-640-32

Query Match	100.0%;	Score 54;	DB 10;	Length 4563;
Best Local Similarity	100.0%;	Pred. No. 1.3;		
Matches	11;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

QY	1	TTRLTRKGLK	11
Db	3384	TTRLTRKGLK	3394

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RESULT 15
US-09-751-708A-128
; Sequence 128. Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASES
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; PRIORITY FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIORITY FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 128
; LENGTH: 4563
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-751-708A-128

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Query Match      100.0%; Score 54; DB 10; Length 4563;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTRLTRRGGK 11
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Db      3584 TTRLTRRGGK 3394

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Search completed: January 12, 2005, 13:52:50
Job time : 89.3548 sec

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2005, 13:13:31 ; Search time 20.2258 Seconds
(without alignments)
52.328 Million cell updates/sec

Title: US-10-657-404A-2
Perfect score: 54
Sequence: 1 TTRLTRKRGK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	596	2 S32802	apolipoprotein B -
2	54	100.0	4563	1 LPHUB	apolipoprotein B-1
3	50	92.6	269	2 C60950	apolipoprotein B-1
4	50	92.6	779	2 JH0102	apolipoprotein B -
5	44	81.5	274	2 A60950	apolipoprotein B-1
6	44	81.5	275	2 B60950	apolipoprotein B-1
7	44	81.5	784	2 JH0101	apolipoprotein B-1
8	43	79.6	309	2 AH0906	conserved hypochet
9	41	75.9	309	1 B65112	hypothetical 34.6
10	41	75.9	309	2 B85985	hypothetical prote
11	41	75.9	309	2 B91140	hypothetical prote
12	38.5	71.3	2073	1 BWA582	bmg protein - Eme
13	38	70.4	1058	2 S65460	apolipoprotein B -
14	38	70.4	1778	2 JY0382	apolipoprotein B -
15	38	70.4	2629	2 I46569	apolipoprotein B -
16	37	68.5	680	2 AB1875	hypothetical prote
17	36	66.7	146	2 T14681	myc-like regulator
18	36	66.7	590	2 E87337	ferrous iron trans
19	35	64.8	124	2 H64221	ribosomal protein
20	35	64.8	305	2 A75334	lacyl-carrier-prot
21	35	64.8	388	1 DEHUP7	pyruvate dehydrog
22	35	64.8	389	1 DEGPA	pyruvate dehydrog
23	35	64.8	390	1 DEHUPA	pyruvate dehydrog
24	35	64.8	390	1 DEHUPA	pyruvate dehydrog
25	35	64.8	390	1 DEHUPA	pyruvate dehydrog
26	35	64.8	390	2 S23506	pyruvate dehydrog
27	35	64.8	689	2 AC1408	transcription anti
28	35	64.8	689	2 AC1784	transcription anti
29	34	63.0	114	2 A90827	hypothetical prote

30	34	63.0	188	2 A87301	MutT/nudix family
31	34	63.0	191	2 E72480	hypothetical prote
32	34	63.0	300	2 AB5532	transposase BME10
33	34	63.0	309	2 AB5538	transposase BME10
34	34	63.0	325	2 T29604	hypothetical prote
35	34	63.0	393	2 S48288	probable phosphor
36	34	63.0	484	2 S40051	starch synthase (E
37	34	63.0	543	2 C66212	hypothetical prote
38	34	63.0	561	1 S34191	suflite reductase
39	34	63.0	857	2 T37459	ribonucleotide red
40	34	63.0	1232	2 T21018	hypothetical prote
41	33	61.1	107	2 S12607	salivary glue prot
42	33	61.1	112	2 S33822	salivary glue prot
43	33	61.1	198	2 T41529	hypothetical prote
44	33	61.1	219	2 A53305	pentose-5-phosphat
45	33	61.1	258	2 T01873	hypothetical prote

ALIGNMENTS

RESULT 1

S32802
apolipoprotein B - crab-eating macaque (fragment)
C.Species: Macaca fascicularis (crab-eating macaque)
C.Date: 06-Jan-1995 #sequence #revision 06-Jan-1995 #text_change 09-Jul-2004
C.Accession: S32802
R.Pape, M.E.; Castle, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.E.; Marotti, K.R.; Melchic
Biochim. Biophys. Acta 1086, 326-334, 1991
A.Title: Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional re
A.Reference number: S32802, MUID:92075708, PMID:1742325
A.Accession: S32802
A>Status: Preliminary
A.Molecule type: mRNA
A.Residues: 1-596 <PAP>
A.Cross-references: UNIPROT:Q28473; EMBL:X15737; NID:G38047; PIDN:CAA3755.1; PID:G93012
C.Superfamily: apolipoprotein B

Query Match 100.0%; Score 54; DB 2; Length 596;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTRLTRKRGK 11
DB 225 TTRLTRKRGK 235

RESULT 2

LPHUB
apolipoprotein B-100 precursor - human
N.Contains: apolipoprotein B-26; apolipoprotein B-48; apolipoprotein B-74
C.Species: Homo sapiens (man)
C.Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text_change 09-Jul-2004
C.Accession: A27850; A25267; A25266; A24320; A24684; A23817; A25774; A26
4452; I61909; I59510; I39474; I39459; I84624; I37179; PS0058
R.Lundwig, B.H.; Blackhart, B.D.; Fierocchi, V.R.; Calati, L.; Fortier, C.; Knott, T.; Sco
DNA 6, 363-372, 1987
A.Title: DNA sequence of the human apolipoprotein B gene.
A.Reference number: A27850, MUID:88003974, PMID:3652907
A.Accession: A27850
A.Molecule type: DNA
A.Residues: 1-617, 'A', 619-1929, 'F', 1931-3318, 'D', 3320-3426, 'T', 3428-3431, 'Q', 3433-3731, '
A.Cross-references: UNIPROT:P04114; UNIPROT:P78482; UNIPROT:P78479; UNIPROT:Q9UMN0; UNIP
R.Cladaras, C.; Hadzopoulos-Cladaras, M.; Nolte, R.T.; Atkinson, D.; Zannis, V.I.
EMBO J. 5, 3495-3507, 1986
A.Title: The complete sequence and structural analysis of human apolipoprotein B-100: re
A.Reference number: A91058, MUID:87161758, PMID:3030729
A.Accession: A25679
A.Molecule type: mRNA
A.Residues: 1-11, 15-2539, 'S', 2541-3823, 'R', 3825-4563 <CIA>
A.Note: 1109-Abp was also found
R.Knott, T.J.; Wallis, S.C.; Powell, L.M.; Pease, R.J.; Lwis, A.J.; Blackhart, B.; McCa
Nucleic Acids Res. 14, 7501-7503, 1986

A>Title: Complete cDNA and derived protein sequence of human apolipoprotein B-100.
A/Reference number: A93639; MUID:87016385; PMID:3763409
A/Accession: A25263
A/Molecule type: mRNA
A/Residues: 1-272, 'N', 274-617, 'A', 619-1217, 'E', 1219-2091, 'V', 2093-2364, 'T', 2366-2679, 'Q'
A/Cross-references: GB:04506; NID:934330; PIDN:CAA8191.1; PID:934331
R/Law, S.W.; Grant, S.M.; Higuchi, K.; Hoshattankar, A.; Lackner, K.; Lee, N.; Brewer JH
Proc. Natl. Acad. Sci. U.S.A. 83, 8142-8146, 1986
A/Title: Human liver apolipoprotein B-100 cDNA: complete nucleic acid and derived amino
A/Reference number: A94134; MUID:87041416; PMID:3464946
A/Accession: A25267
A/Molecule type: mRNA
A/Residues: 1-617, 'A', 619-703, 'P', 705-792, 'R', 794-1270, 'S', 1272-1866, 'G', 1868-2036, 'N', 2
4189-4220, 'W', 4222-4563 <LAW>
A/Note: The codons given for residues 704, 793, 1271, 2037, 2933, 3286, 3782, 4188, and
J. Biol. Chem. 261, 12918-12921, 1986
A/Title: The complete cDNA and amino acid sequence of human apolipoprotein B-100.
A/Reference number: A92556; MUID:87008488; PMID:3759943
A/Accession: A25266
A/Molecule type: mRNA
A/Residues: 1-37, 'I', 99-328, 'V', 330-644, 'I', 646-918, 'P', 920-3318, 'D', 3320-3426, 'T', 3428-
9-4132, 'G', 4134-4180, 'E', 4182-4563 <CH>
A/Cross-references: GB:02610; NID:9378803; PIDN:AAA5549.1; PID:9178804
A/Note: A total of 2366 residues were confirmed by direct sequencing of tryptic peptides
R/Procter, A.A.; Hardman, D.A.; Sato, K.Y.; Schilling, J.W.; Yamana, M.; Hori, Y.; H
Proc. Natl. Acad. Sci. U.S.A. 83, 5678-5682, 1986
A/Title: Analysis of cDNA clones encoding the entire B-26 region of human apolipoprotein
A/Reference number: A24320; MUID:86287319; PMID:3461454
A/Accession: A24320
A/Molecule type: mRNA
A/Residues: 1-97, 'I', 99-617, 'A', 619-941, 'Y', 943-1138, 'P', 1139-1180, 'P', 1181-1219, 'S', 1221-1270, 'S', 1272-1286, 'G', 1288-1318, 'P', 1320-1338, 'D', 1340-1358, 'P', 1360-1378, 'S', 1380-1398, 'P', 1400-1418, 'S', 1420-1438, 'P', 1440-1458, 'S', 1460-1478, 'P', 1480-1498, 'S', 1500-1518, 'P', 1520-1538, 'S', 1540-1558, 'P', 1560-1578, 'S', 1580-1598, 'P', 1600-1618, 'S', 1620-1638, 'P', 1640-1658, 'S', 1660-1678, 'P', 1680-1698, 'S', 1700-1718, 'P', 1720-1738, 'S', 1740-1758, 'P', 1760-1778, 'S', 1780-1798, 'P', 1800-1818, 'S', 1820-1838, 'P', 1840-1858, 'S', 1860-1878, 'P', 1880-1898, 'S', 1900-1918, 'P', 1920-1938, 'S', 1940-1958, 'P', 1960-1978, 'S', 1980-1998, 'P', 2000-2018, 'S', 2020-2038, 'P', 2040-2058, 'S', 2060-2078, 'P', 2080-2098, 'S', 2100-2118, 'P', 2120-2138, 'S', 2140-2158, 'P', 2160-2178, 'S', 2180-2198, 'P', 2200-2218, 'S', 2220-2238, 'P', 2240-2258, 'S', 2260-2278, 'P', 2280-2298, 'S', 2300-2318, 'P', 2320-2338, 'S', 2340-2358, 'P', 2360-2378, 'S', 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A>Note: cysteines at positions 112, 1422, 1505, 1662, 3761, 3917, and 4217 have free su
 R:LeBoeuf, R.C.; Miller, C.; Shively, J.E.; Schumaker, V.N.; Balla, M.A.; Lusis, A.J.
 FEMS Lett. 170, 105-108, 1984
 A:Title: Human apolipoprotein B: partial amino acid sequence.
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 A:Reference number: A22006; MUID:84208786; PMID:6373369
 A:Accession: A22006
 A:Molecule type: protein
 A:Residues: 873-892, 'K', 894-896 <LE1>
 A:Accession: B22006
 A:Molecule type: protein
 A:Residues: 3113, 'L', 3115-3130, 'R', 3132-3133, 'P', 3135-3136, 'R' <LE2>
 R:Blackhart, B.D.; Ludwig, E.M.; Pietrocci, V.R.; Calafati, L.; Onasch, M.A.; Wallis, S.C.;
 J. Biol. Chem. 261, 15364-15367, 1986
 A:Title: Structure of the human apolipoprotein B gene.
 A:Reference number: A92564; MUID:87057153; PMID:2946672
 A:Contents: annotation; gene structure
 R:Wagener, R.; Piltzner, R.; Stoffel, W.
 Biol. Chem. Hoppe-Seyler 368, 419-425, 1987
 A:Title: Studies on the organization of the human apolipoprotein B 100 gene.
 A:Reference number: A90715; MUID:87271140; PMID:2886136
 A:Contents: annotation; gene structure
 R:Weisgraber, K.H.; Rall Jr., S.C.
 J. Biol. Chem. 262, 11097-11103, 1987
 A:Title: Human apolipoprotein B-100 heparin-binding sites.
 A:Reference number: A92605; MUID:87280197; PMID:3301850
 A:Contents: annotation; heparin binding and disulfide bond
 R:Dacht, N.; Lee, D.M.; Mok, T.
 Biochem. Biophys. Res. Commun. 137, 493-499, 1986
 A:Title: Apolipoprotein B is a calcium binding protein.
 A:Reference number: A90125; MUID:86242245; PMID:3087360
 A:Contents: annotation; calcium binding
 R:Carlsson, P.; Olofsson, S.O.; Bondjers, G.; Darnfors, C.; Wiklund, O.; Bjursell, G.
 Nucleic Acids Res. 13, 8813-8826, 1985
 A:Title: Molecular cloning of human apolipoprotein B cDNA.
 A:Reference number: I37178; MUID:86093680; PMID:3841204
 A:Accession: I37180

Query Match 100.0%; Score 54; DB 1; Length 4563;
 Best Local Similarity 100.0%; Pred. No. 0.091;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTRLTRKRGK 11
 |||||
 Db 3384 TTRLTRKRGK 3394

RESULT 3

Apolipoprotein B-100 - golden hamster (fragment)
 C:Species: Mesocricetus auratus (golden hamster)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 A:Accession: C60950
 R:Law, A.; Scott, J.
 J. Lipid Res. 31, 1109-1120, 1990
 A:Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL
 A:Reference number: A60950; MUID:90324804; PMID:2373961
 A:Accession: C60950
 A:Molecule type: DNA
 A:Residues: 1-269 <LAW>
 A:Cross-references: UNIPROT:O60537; UNIPROT:O60536
 C:Superfamily: apolipoprotein B
 C:Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;

Query Match 92.6%; Score 50; DB 2; Length 269;
 Best Local Similarity 90.9%; Pred. No. 0.044;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTRLTRKRGK 11
 |||||
 Db 215 TTRLTRKRGK 225

RESULT 4

JH0102
 apolipoprotein B - golden hamster (fragment)
 C:Species: Mesocricetus auratus (golden hamster)
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
 A:Accession: JH0102
 R:Smith, T.J.
 submitted to GenBank, June 1990
 A:Reference number: A38864
 A:Accession: JH0102
 A:Molecule type: DNA
 A:Residues: 1-779 <SM1>
 A:Cross-references: UNIPROT:O60536; GB:M35187
 A>Note: this is a revision to the sequence from reference JH0101
 R:Smith, T.J.; Hautama, D.; Maeda, N.
 Gene 87, 309-310, 1990
 A:Title: Sequence of the putative low-density lipoprotein receptor-binding regions of ap
 A:Reference number: JH0101; MUID:90236327; PMID:2332175
 A:Contents: annotation
 A>Note: this sequence has been revised in reference A38864
 C:Genetics:
 A:Gene: apob
 C:Superfamily: apolipoprotein B
 C:Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein,
 F:435-445/Region: receptor binding
 F:646-656/Region: receptor binding

Query Match 92.6%; Score 50; DB 2; Length 779;
 Best Local Similarity 90.9%; Pred. No. 0.11;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTRLTRKRGK 11
 |||||
 Db 641 TTRLTRKRGK 651

RESULT 5

Apolipoprotein B-100 - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 31-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
 A:Accession: A60950
 R:Law, A.; Scott, J.
 J. Lipid Res. 31, 1109-1120, 1990
 A:Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL
 A:Reference number: A60950; MUID:90324804; PMID:2373961
 A:Accession: A60950
 A:Molecule type: mRNA
 A:Residues: 1-274 <LAW>
 A:Cross-references: UNIPROT:Q7W2U9
 A>Note: authors translated the codon GAT for residue 155 as His
 C:Superfamily: apolipoprotein B
 C:Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein,

Query Match 81.5%; Score 44; DB 2; Length 274;
 Best Local Similarity 81.8%; Pred. No. 0.66;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 TTRLTRKRGK 11
 |||||
 Db 220 TTRLTRKRGK 230

RESULT 6

Apolipoprotein B-100 - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 A:Accession: E60950
 R:Law, A.; Scott, J.
 J. Lipid Res. 31, 1109-1120, 1990
 A:Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL
 A:Reference number: A60950; MUID:90324804; PMID:2373961
 A:Accession: E60950

A:Molecule type: mRNA
 A:Residues: 1-275 <LAW>
 A:Cross-references: UNIPROT:Q7L277
 C:Superfamily: apolipoprotein B
 C:Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;

Query Match
 Best Local Similarity 81.5%; Score 44; DB 2; Length 275;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db
 220 TSLTRKRGK 230

RESULT 7

JH0101
 apolipoprotein B-100 - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
 C:Accession: JH0101; S3128; D60950
 R:Smith, T.J.; Hautamaa, D.; Maeda, N.
 Gene 87, 309-310, 1990
 A:Title: Sequence of the putative low-density lipoprotein receptor-binding regions of ap

A:Accession: JH0101; MUID:90236327; PMID:2332175
 A:Molecule type: DNA
 A:Residues: 1-784 <SMT>
 A:Cross-references: UNIPROT:Q61314; GB:M35186
 R:Smith, T.; Hautamaa, D.; Maeda, N.
 submitted to the EMBL Data Library, May 1989
 A:Reference number: S3128
 A:Accession: S3128
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-531 'S', 533-784 <SM2>
 A:Cross-references: EMBL:X15191
 R:Law, A.; Scott, J.
 J. Lipid Res. 31, 1109-1120, 1990
 A:Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL

A:Reference number: A60950; MUID:90324604; PMID:2373961
 A:Molecule type: mRNA
 A:Residues: 427-531 'S', 533-700 <LAW>
 C:Genetics:
 A:Gene: MGI:Apob
 A:Cross-references: MGI:88052
 C:Superfamily: apolipoprotein B
 C:Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
 F:435-445/Region: receptor binding
 F:646-656/Region: receptor binding

Query Match
 Best Local Similarity 81.5%; Score 44; DB 2; Length 784;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db
 646 TSLTRKRGK 656

RESULT 8

AH0906
 conserved hypothetical protein STY3508 [imported] - Salmonella enterica subsp. enterica
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C:Accession: AH0906
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Mout, S.; O'Geary, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A:Reference number: A60502; MUID:21534947; PMID:11677608
 A:Accession: AH0906
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-309 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD07846.1; PID:G16504394; GSPDB:GN00176
 C:Genetics:
 A:Gene: STY3508
 C:Superfamily: Methanococcus jannaschii conserved hypothetical protein M0486

Query Match
 Best Local Similarity 79.6%; Score 43; DB 2; Length 309;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db
 169 TTRLRKRGK 179

RESULT 9

E65112
 hypothetical 34.6 kD protein in arcB-glcB intergenic region - Escherichia coli (strain :
 C:Species: Escherichia coli
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: E65112
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M., cc
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617; PMID:9278503
 A:Accession: E65112
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-309 <BLAT>
 A:Cross-references: UNIPROT:P45476; GB:AE000400; GB:U00096; NID:G2367203; PIDN:AACT62a
 A:Experimental source: strain K-12, substrain MG1655
 C:Genetics:
 A:Gene: yhcC
 C:Superfamily: Methanococcus jannaschii conserved hypothetical protein M0486

Query Match
 Best Local Similarity 75.9%; Score 41; DB 1; Length 309;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db
 169 TTRLRKRGK 179

RESULT 10

E83985
 hypothetical protein yhcC [imported] - Escherichia coli (strain O157:H7, substrain EDL9
 C:Species: Escherichia coli
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C:Accession: E83985
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: E83985
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-309 <STO>
 A:Cross-references: UNIPROT:P45476; GB:AE005174; NID:G12517832; PIDN:AA658345.1; GSPDB:G

C:Genetics:
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Gene: yhcC
 C:Superfamily: Methanococcus jannaschii conserved hypothetical protein M0486

Query Match
 Best Local Similarity 75.9%; Score 41; DB 2; Length 309;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11

Db 169 TTOLARORGLK 179

RESULT 11

B91140
hypothetical protein ECs4090 [imported] - Escherichia coli (strain O157:H7, substrain R1)

C:Species: Escherichia coli

C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C:Accession: B91140

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc

A:Reference number: A96629; MUID:21156231; PMID:11258796

A:Accession: B91140

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-309 <HAV>

A:Cross-references: UNIPROT:P45476; GB:BA000007; PIDN:BA037513.1; PID:g13363563; GSPDB:C

A:Experimental source: strain O157:H7, substrain R1MD 0509952

C:Genetics:

A:Gene: ECs4090

C:Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486

Query Match 75.9%; Score 41; DB 2; Length 309;

Best Local Similarity 72.7%; Pred. No. 2.8;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11

Db 169 TTOLARORGLK 179

RESULT 12

BWABSE
bime protein - Emericella nidulans

C:Species: Emericella nidulans, Aspergillus nidulans

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C:Accession: A37879

R:Engle, D.B.; Osmann, S.A.; Osmann, A.H.; Rosborough, S.; Xiang, X.; Morris, N.R.

J. Biol. Chem. 265, 16132-16137, 1990

A:Title: A negative regulator of mitosis in Aspergillus is a putative membrane-spanning

A:Reference number: A37879; MUID:90375468; PMID:1697851

A:Accession: A37879

A:Molecule type: mRNA

A:Residues: 1-2073 <ENG>

A:Cross-references: UNIPROT:P24686; GB:M59705; GB:J05607; NID:g168026; PIDN:AAA51478.1;

A:Note: In addition to three predicted transmembrane domains, there are several potential

asein kinases, and one sequence that resembles a nuclear localization signal

C:Comment: This protein is part of a regulatory pathway that includes the nima protein k

ter mitosis and prevent them from leaving mitosis.

C:Genetics:

A:Gene: bime

C:Superfamily: bime protein

C:Keywords: cell cycle control; mitosis; transmembrane protein

F:163-1643/Domain: transmembrane #status predicted <TM1>

F:165-1703/Domain: transmembrane #status predicted <TM2>

F:1746-1764/Domain: transmembrane #status predicted <TM3>

Query Match 71.3%; Score 38.5; DB 1; Length 2073;

Best Local Similarity 90.9%; Pred. No. 47;

Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 TTRLTRKRGK 10

Db 831 TTRLTRKRGK 841

RESULT 13

S65460

apolipoprotein B - Atlantic salmon (fragment)

C:Species: Salmo salar (Atlantic salmon)

C:Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004

C:Accession: S65460; I51362

R:Babin, P.J.; Deryckere, F.; Gannon, F.

Eur. J. Biochem. 230, 45-51, 1995

A:Title: Presence of an extended duplication in the putative low-density lipoprotein rec

A:Reference number: I51362; MUID:95324549; PMID:7541349

A:Accession: S65460

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-1058 <BAB>

A:Cross-references: UNIPROT:Q91480; EMBL:X81856; NID:9854619; PIDN:CAA57449.1; PID:g8546

A:Experimental source: liver

C:Genetics:

A:Gene: apob

C:Superfamily: apolipoprotein B

C:Keywords: calcium; cholesterol metabolism; chylomicron; glycoprotein; intestine; LDL;

Query Match 70.4%; Score 38; DB 2; Length 1058;

Best Local Similarity 72.7%; Pred. No. 32;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11

Db 501 TSLTRKRGK 511

RESULT 14

JT0382
apolipoprotein B - pig (fragments)

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C:Accession: JT0382; I46567; I46568

R:Maeda, N.; Ebert, D.L.; Doers, T.M.; Newman, M.; Hasler-Rapacz, J.; Attie, A.D.; Rapac

Gene 70, 213-229, 1988

A:Title: Molecular genetics of the apolipoprotein B gene in pigs in relation to atheros

A:Reference number: JT0382; MUID:89108006; PMID:2905687

A:Accession: JT0382

A:Molecule type: DNA

A:Residues: 1-1778 <MAE>

A:Cross-references: UNIPROT:Q29020; UNIPROT:Q29433

R:Maeda, N.; Ebert, D.L.; Doers, T.M.; Newman, M.; Hasler-Rapacz, J.O.; Attie, A.D.; Rap

Gene 69, 213-229, 1988

A:Title: Molecular genetics of the apolipoprotein B gene in pigs in relation to atheros

A:Reference number: I46567

A:Accession: I46567

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-8, 'S', '10-238 <MA2>

A:Cross-references: GB:M2647; NID:g164367; PIDN:AAA30996.1; PID:g164369

A:Accession: I46568

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 239-1778 <MA3>

A:Cross-references: GB:M2647; NID:g164367; PIDN:AAA30997.1; PID:g164370

C:Comment: Apolipoprotein B is the predominant protein component of the low-density lipop

C:Genetics:

A:Gene: apob

A:Introns: 39/3; 88/3; 159/2; 238/3; 1133/1; 1171/2; 1232/3

A:Note: The list of introns may be incomplete

C:Superfamily: apolipoprotein B

C:Keywords: atherosclerosis; cholesterol metabolism; LDL; lipid binding; lipoprotein

Query Match 70.4%; Score 38; DB 2; Length 1778;

Best Local Similarity 72.7%; Pred. No. 51;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11

Db 588 TSLTRKRGK 598

RESULT 15

I46569

apolipoprotein B - pig (fragment)

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004

C/Accession: I46569

R/Putrell, C.; Maeda, N.; Ebert, D.L.; Kaiser, M.; Lund-Katz, S.; Sturley, S.L.; Kodoyiad

J.; Lipid Res. 34, 1323-1335, 1993

A/Title: Nucleotide sequence encoding the carboxyl-terminal half of apolipoprotein B fr

A/Reference number: I46569; KUID:94014802; PMID:8409766

A/Accession: I46569

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-2629 <PUR>

C/Cross-references: UNIPROT:Q29021; GB:I11235; NID:G164371; PID:AAA74655.1; PID:G951375

A/Genes: APOB

C/Intons: 1984/1; 2022/2; 2083/3

C/Superfamily: apolipoprotein B

Query Match

Best Local Similarity 70.4%; Score 38; DB 2; Length 2629;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTRLTRKRGK 11

Db 1438 TSLMKRRGK 1448

Search completed: January 12, 2005, 13:31:57

Job time : 21.2258 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2005, 12:49:11 ; Search time 109.645 Seconds
(without alignments)
57.724 Million cell updates/sec

Title: US-10-657-404A-2
Perfect score: 54
Sequence: 1 TTRLTRKRGK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	414	2 QYOR5	QYQF5 aotus vocif
2	54	100.0	596	2 Q28473	Q28473 macaca fasc
3	54	100.0	3262	2 Q13788	Q13788 homo sapien
4	54	100.0	4563	1 APB_HUMAN	P04114 homo sapien
5	54	100.0	4563	2 Q2600	Q26000 homo sapien
6	50	92.6	421	2 Q7TN68	Q7TN68 glaucomye v
7	50	92.6	432	2 Q7YR10	Q7YR10 diceros bic
8	50	92.6	436	2 Q7YOM8	Q7YOM8 nyctimene a
9	50	92.6	438	2 Q7YOM7	Q7YOM7 pteropus hy
10	50	92.6	438	2 Q7YR04	Q7YR04 roussetus a
11	50	92.6	445	2 Q7YR08	Q7YR08 chaetophrac
12	50	92.6	445	2 Q7TN64	Q7TN64 agouti paca
13	50	92.6	445	2 Q7TN71	Q7TN71 hydrochoeru
14	50	92.6	445	2 Q7TN72	Q7TN72 etehizon d
15	50	92.6	780	2 Q60536	Q60536 mesocricetu
16	50	92.6	780	2 Q60537	Q60537 mesocricetu
17	48	88.9	387	2 Q7YON2	Q7YON2 phalangero
18	48	88.9	445	2 Q7TN70	Q7TN70 dinomys bra
19	47	87.0	407	2 Q7TN65	Q7TN65 athemurus a
20	47	87.0	412	2 Q7TN69	Q7TN69 hystrix bra
21	44	81.5	274	2 Q7M2U9	Q7M2U9 otycolagus
22	44	81.5	275	2 Q7L277	Q7L277 gallus galli
23	44	81.5	304	2 Q7YOP9	Q7YOP9 eichomys te
24	44	81.5	314	2 Q7YON8	Q7YON8 icomys scr
25	44	81.5	316	2 Q7YOP3	Q7YOP3 nandania bi
26	44	81.5	318	2 Q7YON9	Q7YON9 zalophus ca
27	44	81.5	319	2 Q7YOP0	Q7YOP0 vulpes vulp
28	44	81.5	319	2 Q7YOP2	Q7YOP2 panthera le
29	44	81.5	320	2 Q7YOP4	Q7YOP4 panis sp. k
30	44	81.5	361	2 Q7YOP8	Q7YOP8 amblyomus
31	44	81.5	386	2 Q7YOR1	Q7YOR1 tupia tana

32	44	81.5	392	2 Q7YR11	Q7YR11 tarsius byr
33	44	81.5	411	2 Q7YOP7	Q7YOP7 ochotona pr
34	44	81.5	422	2 Q7YR12	Q7YR12 talpa europ
35	44	81.5	423	2 Q7YQ92	Q7YQ92 sorex monti
36	44	81.5	426	2 Q7YOR2	Q7YOR2 alces alces
37	44	81.5	429	2 Q7YQ08	Q7YQ08 crocidura f
38	44	81.5	438	2 Q7YOR4	Q7YOR4 balaena myr
39	44	81.5	441	2 Q7YOR3	Q7YOR3 phocoenoid
40	44	81.5	443	2 Q7YON5	Q7YON5 megaderma l
41	44	81.5	443	2 Q7YOP6	Q7YOP6 lepus ameri
42	44	81.5	445	2 Q7YON6	Q7YON6 bradypus tr
43	44	81.5	445	2 Q7YQ07	Q7YQ07 capinus bai
44	44	81.5	445	2 Q7YOR0	Q7YOR0 cynocephalu
45	44	81.5	445	2 Q7YR07	Q7YR07 lemur catca

ALIGNMENTS

RESULT 1					
ID	QYOR5	PRELIMINARY;	PRT;	414 AA.	
AC	QYOR5;				
DT	01-OCT-2003 (TREMBlrel. 25, Created)				
DT	01-OCT-2003 (TREMBlrel. 25, Last sequence update)				
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)				
DE	Apollipoprotein B 100 (Fragment).				
GN	Name=apob-100;				
OS	Aotus vociferans (Spix's owl monkey).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.				
OX	NCBI_TaxID=57176;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=22761261; PubMed=12878460;				
RA	Amitine-Madsen H., Koefli K.-P., Wayne R.K., Springer M.S.;				
RT	"A new phylogenetic marker, apollipoprotein B, provides compelling				
RT	evidence for eutherian relationships."				
RL	Mol. Phylogenet. Evol. 28:225-240(2003).				
DR	EMBL; AF548396; AAP9352.1; -.				
KW	Lipoprotein.				
FT	NON_TER	1	1		
FT	NON_TER	414	414		
SQ	SEQUENCE	414 AA;	45955 MW;	EEFA8492157E1BDE CRC64;	
Query Match					
Best Local Similarity 100.0%; Score 54; DB 2; Length 414;					
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1 TTRLTRKRGK 11				
DB	257 TTRLTRKRGK 267				
RESULT 2					
ID	Q28473	PRELIMINARY;	PRT;	596 AA.	
AC	Q28473;				
DT	01-NOV-1996 (TREMBlrel. 01, Created)				
DT	01-NOV-1996 (TREMBlrel. 01, Last sequence update)				
DT	01-JUN-2003 (TREMBlrel. 24, Last annotation update)				
DE	Apollipoprotein B (Fragment).				
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;				
OC	Cercopitheidae; Macaca.				
OX	NCBI_TaxID=9541;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Liver;				
RX	MEDLINE=92075708; PubMed=1742325;				
RA	Pape M.E., Castle C.K., Murray R.W., Funk G.M., Hunt C.E.,				
RA	Marotit K.R., Melchior G.W.;				

RT "Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional regulation."
 RL Biochim. Biophys. Acta 1086:326-334 (1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Murray R.;

RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X15737; CAA3755.1; -.
 DR PIR; S32802; S32802.
 KW Lipoprotein.
 FT NON_TER
 SQ SEQUENCE 596 AA; 66757 MW; B13BA74E25C3120 CRC64;

Query Match 100.0%; Score 54; DB 2; Length 596;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTRLTTRKRGK 11
 Db 225 TTRLTTRKRGK 235

RESULT 3
 ID 013788 PRELIMINARY; PRT; 3262 AA.
 AC 013788;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DE 01-UN-2003 (TRENBLrel. 24, Last annotation update)
 GN APOB protein (Fragment).
 OS Name=APOB;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=87191999; PubMed=2883086;
 RA Carlsson P., Darntors C., Olofsson S.O., Bjureell G.,
 RT "Analysis of the human apolipoprotein B gene; complete structure of
 RL the B-74 region."
 DR EMBL; M15421; AAS1758.1; -.
 DR PIR; A27850; LPHUB.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0005319; F:lipid transporter activity; NAS.
 DR GO; GO:0008669; P:lipid transport; NAS.
 FT NON_TER
 SQ SEQUENCE 3262 AA; 370140 MW; 56603BC0618DD40D CRC64;

Query Match 100.0%; Score 54; DB 2; Length 3262;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTRLTTRKRGK 11
 Db 2083 TTRLTTRKRGK 2093

RESULT 4
 APB_HUMAN STANDARD; PRT; 4563 AA.
 ID APB_HUMAN
 AC P04114; 000502; 013787;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 05-JUL-2004 (Rel. 03, Last sequence update)
 DE Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipoprotein
 DE B-48 (Apo B-48)].
 GN Name=APOB;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=87016385; PubMed=3763409;
 RA Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.,
 RA Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.,
 RT "Complete cDNA and derived protein sequence of human apolipoprotein B-
 RT 100.";
 RL Nucleic Acids Res. 14:7501-7503 (1986).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANT GLU-4181.
 RA MEDLINE=86003974; PubMed=3652907;
 RA Ludwig E.H., Blackhart B.D., Pierotti V.R., Caiati L., Fortier C.,
 RA Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.,
 RT "DNA sequence of the human apolipoprotein B gene.";
 RL DNA 6:363-372 (1987).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANTS ILE-98 AND GLU-4181.
 RA MEDLINE=87008489; PubMed=3759943;
 RA Chen S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,
 RA Goto A.M., Jr., Chan L.;
 RT "The complete cDNA and amino acid sequence of human apolipoprotein B-
 RT 100.";
 RL J. Biol. Chem. 261:12918-12921 (1986).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=87041416; PubMed=3464946;
 RA Law S.W., Grant S.M., Higuchi K., Hospattankar A.V., Lackner K.J.,
 RA Lee N., Brewer H.B., Jr.;
 RT "Human liver apolipoprotein B-100 cDNA: complete nucleic acid and
 RT derived amino acid sequence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146 (1986).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=87161758; PubMed=3030729;
 RA Cladaras C., Hadzopoulou-Cladaras M., Nolte R.T., Atkinson D.,
 RA Zannis V.I.;
 RT "The complete sequence and structural analysis of human apolipoprotein
 RT B-100: relationship between apob-100 and apob-48 forms.";
 RL EMBO J. 5:3495-3507 (1986).
 RN [6]
 RP SEQUENCE OF 709-906 FROM N.A.
 RA MEDLINE=85270450; PubMed=3860836;
 RA Deep S.S., Motulsky A.G., Albers J.J.;
 RT "A partial cDNA clone for human apolipoprotein B.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986 (1985).
 RN [7]
 RP SEQUENCE OF 3056-3159 FROM N.A.
 RA MEDLINE=86041888; PubMed=3903560;
 RA Weinribian M., Schumaker V.N., Fareed G.C., West R., Johnson D.F.,
 RA Kirchgessner T.G., Lin H.-C., Wang X., Ma Y., Mendiaz B., Lusis A.J.;
 RT "Human apolipoprotein B: identification of cDNA clones and
 RT characterization of mRNA.";
 RL Nucleic Acids Res. 13:6937-6953 (1985).
 RN [8]
 RP SEQUENCE OF 1937-2018 AND 3811-4334 FROM N.A., AND VARIANT GLU-4181.
 RA MEDLINE=86093680; PubMed=3841204;
 RA Carlsson P., Olofsson S.O., Bondjers G., Darntors C., Wiklund O.,
 RA Bjureell G.;
 RT "Molecular cloning of human apolipoprotein B cDNA.";
 RL Nucleic Acids Res. 13:6813-6826 (1985).
 RN [9]
 RP SEQUENCE OF 3109-4563 FROM N.A.
 RA MEDLINE=85300528; PubMed=2994225;
 RA Knott T.J., Rall S.C., Jr., Innerarity T.L., Jacobson S.F., Urdea M.S.,
 RA Levy-Wilson B., Powell L.M., Pease R.J., Bddy R., Nakai H., Byers M.,
 RA Priestley L.M., Robertson E., Rall L.B., Betsholtz C., Shows T.B.,
 RA Mahley R.W., Scott J.;
 RT "Human apolipoprotein B: structure of carboxyl-terminal domains, sites
 RT of gene expression, and chromosomal localization.";
 RL Science 230:37-43 (1985).
 RN [10]

RP SEQUENCE OF 1-291 FROM N.A.
 RX MEDLINE=86149325; PubMed=351317;
 RA Procter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V.,
 RA Chen G.C., Kirschner S.W., McEnroe G., Kane J.P.;
 RT "Isolation of a cDNA clone encoding the amino-terminal region of human
 RT apolipoprotein B.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:1467-1471(1986).
 [11]
 RP SEQUENCE OF 1-1670 FROM N.A., AND VARIANT IIE-98.
 RX MEDLINE=86287319; PubMed=3461454;
 RA Procter A.A., Hardman D.A., Sato K.Y., Schilling J.W., Yamanaka M.,
 RA Hori Y.J., Hjerrild K.A., Chen G.C., Kane J.P.;
 RT "Analysis of cDNA clones encoding the entire B-26 region of human
 RT apolipoprotein B.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682(1986).
 [12]
 RP PARTIAL SEQUENCE, AND IDENTIFICATION OF APO-B48.
 RX MEDLINE=86018019; PubMed=3559919;
 RA Chen S.-H., Habib G., Yang C.-H., Gu Z.-W., Lee B.-R., Weng S.-H.,
 RA Silbermann S.R., Cai S.-J., Deslypere J.P., Roseneau M.,
 RA Gotto A.M. Jr., Li W.-H., Chan L.;
 RT "Apolipoprotein B-48 is the product of a messenger RNA with an organ-
 RT specific in-frame stop codon.";
 RL Science 238:363-366(1987).
 [13]
 RP DOMAINS.
 RX MEDLINE=87039351; PubMed=3773997;
 RA Knott T.C., Pease R.J., Powell L.M., Wallis S.C., Rall S.C. Jr.,
 RA Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R.,
 RA Johnson D., Fuller M., Lusis A.J., McCarthy B.J., Mahley R.W.,
 RA Levy-Wilson B., Scott J.;
 RT "Complete protein sequence and identification of structural domains of
 RT human apolipoprotein B.";
 RL Nature 323:734-738(1986).
 [14]
 RP DOMAINS.
 RX MEDLINE=87039351; PubMed=3773997;
 RA Yang C.-Y., Chen S.-H., Gianturco S.H., Bradley W.A., Sparrow J.T.,
 RA Tanihara M., Li W.-H., Sparrow D.A., Deloof H., Roseneau M.,
 RA Lee F.-S., Gu Z.-W., Gotto A.M. Jr., Chan L.;
 RT "Sequence, structure, receptor-binding domains and internal repeats of
 RT human apolipoprotein B-100.";
 RL Nature 323:738-742(1986).
 [15]
 RP CALCIUM-BINDING DATA.
 RX MEDLINE=86242245; PubMed=3087360;
 RA Dashti N., Lee D.M., Mok T.;
 RT "Apolipoprotein B is a calcium binding protein.";
 RL Biochem. Biophys. Res. Commun. 137:493-499(1986).
 [16]
 RP PALMITOYLATION OF CYS-1112.
 RX MEDLINE=20143590; PubMed=10679026;
 RA Zhao Y., McCabe J.B., Vance J., Berthiaume L.G.;
 RT "Palmitoylation of apolipoprotein B is required for proper
 RT intracellular sorting and transport of cholesterol esters and
 RT triglycerides.";
 RL Mol. Biol. Cell 11:721-734(2000).
 [17]
 RP VARIANT SER-4338.
 RX MEDLINE=91071750; PubMed=1979313;
 RA Navajas M., Laurent A.-M., Morel J.-F., Ragab A., Cambou J.-P.,
 RA Cuny G., Cambien F., Roizes G.;
 RT "Detection by denaturing gradient gel electrophoresis of a new
 RT polymorphism in the apolipoprotein B gene.";
 RL Hum. Genet. 86:91-93(1990).
 [18]
 RP VARIANT FDB GLN-1527.
 RX MEDLINE=89098975; PubMed=2563166;
 RA Sorta L.F., Ludwig E.H., Clarke H.R.G., Vega G.L., Grundy S.M.,
 RA McCarthy B.J.;
 RT "Association between a specific apolipoprotein B mutation and familial
 RT defective apolipoprotein B-100.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).
 [19]

RP VARIANT LEU-2739.
 RX MEDLINE=91016874; PubMed=2216805;
 RA Huang L.-S., Gavish D., Breslow J.L.;
 RT "Sequence polymorphism in the human apob gene at position 8344.";
 RL Nucleic Acids Res. 18:5922-5922(1990).
 [20]
 RP VARIANT FDB CYS-3558.
 RX MEDLINE=95190020; PubMed=7083971;
 RA Pullinger C.R., Hennessy L.K., Chatterton J.E., Liu W., Love J.A.,
 RA Mendel C.M., Frost P.H., Malloy M.J., Schumaker V.N., Kane J.P.;
 RT "Familial ligand-defective apolipoprotein B. Identification of a new
 RT mutation that decreases LDL receptor binding affinity.";
 RL J. Clin. Invest. 95:1225-1234(1995).
 [21]
 RP VARIANTS LEU-1437, SER-1914, LYS-2566, THR-3121, ALA-3945, MET-4128
 RP AND THR-4481.
 RX MEDLINE=97044521; PubMed=8889592;
 RA Pollier O., Ricard S., Behague I., Souriau C., Evans A.E.,
 RA Arveiler D., Marques-Vidal P., Luc G., Roizes G., Cambien F.;
 RT "Detection of new variants in the apolipoprotein B (apo B) gene by
 RT PCR-SSCP.";
 RL Hum. Mutat. 8:282-285(1996).
 [22]
 RP VARIANTS FDB GLN-3527 AND CYS-3558.
 RX MEDLINE=97403938; PubMed=9259199;
 RA Rabes J.P., Varret M., Saint-Jore B., Erlich D., Jondeau G.,
 RA Krampe M., Giraudet P., Junien C., Boileau C.;
 RT "Familial ligand-defective apolipoprotein B-100: simultaneous
 RT detection of the ARG3500->GLN and ARG3531->CYS mutations in a French
 RT population.";
 RL Hum. Mutat. 10:160-163(1997).
 [23]
 RP VARIANTS SER-1914, ARG-1923, LEU-2739, ASP-3319, THR-3427, GLN-3432
 RP AND ILE-3921.
 RX MEDLINE=98141125; PubMed=9490296;
 RA Leren T.P., Bakken K.S., Hoel V., Hjermann I., Berg K.;
 RT "Screening for mutations of the apolipoprotein B gene causing
 RT hypocholesterolemia.";
 RL Hum. Genet. 102:44-49(1998).
 CC -I- FUNCTION: Apolipoprotein B is a major protein constituent of
 CC chylomicrons (apo B-48), LDL (apo B-100) and VLDL (apo B-100). Apo
 CC B-100 functions as a recognition signal for the cellular binding
 CC and internalization of LDL particles by the apoB/E receptor.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 Query Match 100.0%; Score 54; DB 1; Length 4563;
 Best Local Similarity 100.0%; Pred. No. 0.42;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTRLRKRGK 11
 DB 3384 TTRLRKRGK 3394
 RESULT 5
 Q72600 PRELIMINARY; PRT; 4563 AA.
 AC Q72600;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Apolipoprotein B (Including Ag(X) antigen).
 GN Name=APOB;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
 RA Ahearn M.O., Kuidanek S.A., Rajkumar N., Toch E.J., Yi Q.,
 RA Nickerson D.A.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY24608; AAF72970.1; -
 DR GO: GO:000519; F:lipid transporter activity; IEA.
 DR GO: GO:0006869; P:lipid transport; IEA.
 DR InterPro: IPR009454; DUF1081.
 DR InterPro: IPR001747; Lipid_transprt_N.
 DR Pfam: PF06448; DUF1081; 1.
 DR Pfam: PF01347; Vitellinogenin_N; 1.
 DR SMART: SM00638; LPD_N; 1.
 DR Lipoprotein.
 KW
 SQ SEQUENCE 4563 AA; 515553 MW; 030B34167CEDC63C CRC64;

Query Match 100.0%; Score 54; DB 2; Length 4563;
 Best Local Similarity 100.0%; Pred. No. 0.42;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTRLTRKRGK 11
 DB 3384 TTRLTRKRGK 3394

RESULT 6

O7TN68 ID O7TN68 PRELIMINARY; PRT; 421 AA.
 AC O7TN68;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Apolipoprotein B (Fragment).
 OS Glaucomys volans (Southern flying squirrel).
 OC Mammalia; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Eukaryota; Eutheria; Rodentia; Sciurognathi; Sciuridae; Petauristinae;
 OC Glaucomys.
 OC NCB1_Taxid=64683;
 RN
 RP
 RX MEDLINE=22761261; PubMed=12878460;
 RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
 RT "A new phylogenetic marker, apolipoprotein B, provides compelling
 RT evidence for eutherian relationships.";
 RL Mol. Phylogenet. Evol. 28:225-240(2003).
 DR EMBL: AY243379; AAP50767.1; -
 KW Lipoprotein.
 FT NON TER 1
 FT NON TER 421
 SQ SEQUENCE 421 AA; 46747 MW; D47B77BD4F864FD1 CRC64;

Query Match 92.6%; Score 50; DB 2; Length 421;
 Best Local Similarity 90.9%; Pred. No. 0.22;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTRLTRKRGK 11
 DB 263 TTRLTRKRGK 273

RESULT 7

O7YR10 ID O7YR10 PRELIMINARY; PRT; 432 AA.
 AC O7YR10;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Apolipoprotein B (Fragment).
 OS Dicerus bicornis (Black rhinoceros).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Dicerus.
 OC NCB1_Taxid=9805;
 RN
 RP
 RX MEDLINE=22761261; PubMed=12878460;
 RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
 RT "A new phylogenetic marker, apolipoprotein B, provides compelling
 RT evidence for eutherian relationships.";

RL Mol. Phylogenet. Evol. 28:225-240(2003).
 DR EMBL: AY243375; AAP50763.1; -
 KW Lipoprotein.
 FT NON TER 1
 FT NON TER 432
 SQ SEQUENCE 432 AA; 48171 MW; F27B7AB39604732C CRC64;

Query Match 92.6%; Score 50; DB 2; Length 432;
 Best Local Similarity 90.9%; Pred. No. 0.22;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTRLTRKRGK 11
 DB 274 TTRLTRKRGK 284

RESULT 8

O7YOM8 ID O7YOM8 PRELIMINARY; PRT; 436 AA.
 AC O7YOM8;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Apolipoprotein B 100 (Fragment).
 OS Nyctimene albigenter (Common tube-nosed fruit bat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
 OC Pteropodidae; Nyctimene.
 OC NCB1_Taxid=46988;
 RN
 RP
 RX MEDLINE=22761261; PubMed=12878460;
 RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
 RT "A new phylogenetic marker, apolipoprotein B, provides compelling
 RT evidence for eutherian relationships.";
 RL Mol. Phylogenet. Evol. 28:225-240(2003).
 DR EMBL: AF548435; AAP97391.1; -
 KW Lipoprotein.
 FT NON TER 1
 FT NON TER 436
 SQ SEQUENCE 436 AA; 48717 MW; 1C4A7EAD72D2C629 CRC64;

Query Match 92.6%; Score 50; DB 2; Length 436;
 Best Local Similarity 90.9%; Pred. No. 0.23;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTRLTRKRGK 11
 DB 278 TTRLTRKRGK 288

RESULT 9

O7YOM7 ID O7YOM7 PRELIMINARY; PRT; 438 AA.
 AC O7YOM7;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Apolipoprotein B 100 (Fragment).
 OS Nyctimene albigenter (Common tube-nosed fruit bat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
 OC Pteropodidae; Nyctimene.
 OC NCB1_Taxid=9405;
 RN
 RP
 RX MEDLINE=22761261; PubMed=12878460;
 RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
 RT "A new phylogenetic marker, apolipoprotein B, provides compelling
 RT evidence for eutherian relationships.";

Mo1. Phylogenet. Evol. 28:225-240(2003).
 DR EMBL: AY243375; AAP50763.1; -
 KW Lipoprotein.
 FT NON TER 1
 FT NON TER 432
 SQ SEQUENCE 432 AA; 48171 MW; F27B7AB39604732C CRC64;

DR EMBL: AF548436; AAP97392.1; --
KW Lipoprotein.
FT NON_TER 1
SQ SEQUENCE 438 AA; 48734 MW; 2BD85BCBF4E2CC41 CRC64;
Query Match
Best Local Similarity 92.6%; Score 50; DB 2; Length 438;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTRLTRKXGK 11
Db 280 TSLRTRKXGK 290
RESULT 10
ID QYR04 PRELIMINARY; PRT; 438 AA.
AC QYR04;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE Apolipoprotein B (Fragment).
OS Roussetus ampelicaudatus (Common roussette).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
OC Pteropodidae; Roussetus.
OX NCBI_TaxID=58083;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22761261; PubMed=12878460;
RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
RT "A new phylogenetic marker, apolipoprotein B, provides compelling
evidence for eutherian relationships.";
RL Mol. Phylogenet. Evol. 28:225-240(2003).
DR EMBL: AY243383; AAP50771.1; --
KW Lipoprotein.
FT NON_TER 1
FT NON_TER 438
SQ SEQUENCE 438 AA; 48597 MW; 41C890DEAF95C872 CRC64;
Query Match
Best Local Similarity 92.6%; Score 50; DB 2; Length 438;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTRLTRKXGK 11
Db 280 TSLRTRKXGK 290
RESULT 11
ID QYR08 PRELIMINARY; PRT; 445 AA.
AC QYR08;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE Apolipoprotein B (Fragment).
OS Chaetopharactes villosus (South American armadillo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Dasypodidae; Chaetopharactes.
OX NCBI_TaxID=29080;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22761261; PubMed=12878460;
RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
RT "A new phylogenetic marker, apolipoprotein B, provides compelling
evidence for eutherian relationships.";
RL Mol. Phylogenet. Evol. 28:225-240(2003).
DR EMBL: AY243378; AAP50766.1; --
KW Lipoprotein.
FT NON_TER 1
FT NON_TER 445
SQ SEQUENCE 445 AA; 445

SQ SEQUENCE 445 AA; 49564 MW; 2DA5DC3ED2F0FD2 CRC64;
Query Match
Best Local Similarity 92.6%; Score 50; DB 2; Length 445;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTRLTRKXGK 11
Db 287 TSLRTRKXGK 297
RESULT 12
ID QYTN64 PRELIMINARY; PRT; 445 AA.
AC QYTN64;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE Apolipoprotein B 100 (Fragment).
CN Name=apob-100;
OS Agouti paca (paca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognath; Agoutidae; Agouti.
OX NCBI_TaxID=108852;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22761261; PubMed=12878460;
RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
RT "A new phylogenetic marker, apolipoprotein B, provides compelling
evidence for eutherian relationships.";
RL Mol. Phylogenet. Evol. 28:225-240(2003).
DR EMBL: AF548417; AAP97373.1; --
KW Lipoprotein.
FT NON_TER 1
FT NON_TER 445
SQ SEQUENCE 445 AA; 49721 MW; 34AF7ABE90F121EF CRC64;
Query Match
Best Local Similarity 92.6%; Score 50; DB 2; Length 445;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTRLTRKXGK 11
Db 287 TSLRTRKXGK 297
RESULT 13
ID QYTN71 PRELIMINARY; PRT; 445 AA.
AC QYTN71;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE Apolipoprotein B (Fragment).
OS Hydrochoerus hydrochaeris (Capybara) (Carpincho).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognath; Hydrochaeridae;
OC Hydrochaeris.
OX NCBI_TaxID=10149;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22761261; PubMed=12878460;
RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
RT "A new phylogenetic marker, apolipoprotein B, provides compelling
evidence for eutherian relationships.";
RL Mol. Phylogenet. Evol. 28:225-240(2003).
DR EMBL: AY243369; AAP50757.1; --
DR InterPro: IPR000871; Beta_lactamase_A.
DR PROSITE: PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
KW Lipoprotein.
FT NON_TER 1
FT NON_TER 445
SQ SEQUENCE 445 AA; 49520 MW; CBBA2DD5D3D7A18D2 CRC64;

Query Match 92.6%; Score 50; DB 2; Length 445;
 Best Local Similarity 90.9%; Pred. No. 0.23;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTRLTRKRGK 11
 ||:|||||||
 DB 287 TSLRTRKRGK 297

RESULT 14

Q7TN72 PRELIMINARY; PRT; 445 AA.

ID Q7TN72
 AC Q7TN72;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DE Apolipoprotein B (Fragment).
 OS Erethizon dorsatum (North American porcupine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Erethizontidae;
 OC Erethizon.
 OX NCBI_TaxID=34844;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22761261; PubMed=12878460;
 RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
 RT "A new phylogenetic marker, apolipoprotein B, provides compelling
 evidence for eutherian relationships."
 RL MBL. Phylogenet. Evol. 28:225-240(2003).
 DR EMBL; AF243368; AAF50756.1; -.
 KW Lipoprotein.
 FT NON_TER 1 445
 FT NON_TER 445
 SQ SEQUENCE 445 AA; 49617 MW; 9572FE5FE7625F2 CRC64;

Query Match 92.6%; Score 50; DB 2; Length 445;
 Best Local Similarity 90.9%; Pred. No. 0.23;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTRLTRKRGK 11
 ||:|||||||
 DB 287 TSLRTRKRGK 297

RESULT 15

ID Q60536 PRELIMINARY; PRT; 780 AA.

AC Q60536;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hamster apolipoprotein (apob) (Fragment).
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90236327; PubMed=2332175;
 RA Smith T.J., Hautamaa D., Maeda N.;
 RT "Sequence of the putative low-density lipoprotein receptor-binding
 regions of apolipoprotein B in mouse and hamster."
 RL Gene 87:309-310(1990).
 DR EMBL; M35187; AAA37059.1; -.
 DR PIR; C60950; C60950.
 DR PIR; JH0102; JH0102.
 KW Lipoprotein.
 FT NON_TER 1 780
 FT NON_TER 780
 SQ SEQUENCE 780 AA; 86625 MW; E371D1B2079D8F7E CRC64;

Query Match 92.6%; Score 50; DB 2; Length 780;
 Best Local Similarity 90.9%; Pred. No. 0.42;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTRLTRKRGK 11
 ||:|||||||
 DB 641 TSLRTRKRGK 651

Search completed: January 12, 2005, 13:30:54
 Job time : 110.645 secs

CC receptor-competent LDL particles do not require the complete apo B
 CC sequence, which is large and tends to aggregate, to provide binding
 CC affinity to an apo B protein receptor
 XX
 SO Sequence 11 AA;

Query Match 100.0%; Score 44; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 RLTRKRGK 9
 Db 3 RLTRKRGK 11

RESULT 2
 AAW57206
 ID AAW57206 standard; peptide; 11 AA.

AC AAW57206;
 XX
 DT 03-AUG-1998 (first entry)
 XX
 DE Apo B 100 binding site peptide analogue peptide A.
 XX
 KW Apo B; binding site; receptor; cancer; drug delivery; anticancer;
 KW growth supplement; non-natural lipid particle; low density lipoprotein;
 KW LDL; receptor component; apo B100 receptor site.
 XX
 OS Synthetic.
 XX

Key Location/Qualifiers
 FT Modified-site 1 /note="attached to retinoic acid"
 FT Modified-site 11 /note="attached to cholesterol"
 XX
 PN W09813385-A2.

PD 02-APR-1998.

PF 25-SEP-1997; 97WO-GB002610.

PR 27-SEP-1996; 96GB-00020153.

PA (UYST) UNIV STRATHCLYDE.

PI Halbert GW, Owens MD, Baillie G;

DR WPI; 1998-230637/20.

PT Non-natural lipid particle comprising peptide binding to apo B protein
 PT receptor - useful as, e.g. vector for delivering drugs to cancer cells
 PT that express this receptor.
 XX

PS Claim 13; Fig 7; 73pp; English.

CC The present sequence represents a specifically claimed Apo B 100 binding
 CC site peptide analogue which can be used as a component of a non-
 CC naturally occurring, receptor-competent low density lipoprotein (LDL)
 CC particle of the present invention. The LDL particle comprises at least 1
 CC peptide component that has at least 1 binding site for an apo B protein
 CC receptor and at least 1 lipophilic substituent. Also described in the
 CC invention are peptides containing an apo B binding sequence with at least
 CC 70% identity with sequences: KAEKKKKHH (1) or TYRLTRKGLK (2), or their
 CC dimers. Non-naturally occurring, receptor-competent LDL particles are
 CC useful as: (i) drug-targeting vectors for delivering anticancer drugs to
 CC cancer cells that express an apo B protein receptor, and (ii) additives
 CC for cell culture media especially as growth supplements. Non-naturally
 CC occurring, receptor-competent LDL particles do not require the complete
 CC apo B sequence, which is large and tends to aggregate, to provide binding
 CC affinity to an apo B protein receptor
 XX

SO Sequence 11 AA;

Query Match 100.0%; Score 44; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 RLTRKRGK 9
 Db 2 RLTRKRGK 10

RESULT 3
 AAW87717
 ID AAW87717 standard; peptide; 11 AA.

AC AAW87717;
 XX
 DT 09-MAR-1999 (first entry)
 XX
 DE Analogue of residues 3359-3369 of apoprotein B 100.
 XX
 KW Analogue; apoprotein B 100; malondialdehyde; MDA; atherosclerosis;
 KW apoprotein B-based low density lipoprotein; LDL; foam cell;
 KW high affinity LDL receptor; cholesterol; epitope.
 XX
 OS Homo sapiens.
 XX

Key Location/Qualifiers
 FT Modified-site 5 /note="conjugated to malondialdehyde (MDA)"
 FT Modified-site 5 /note="conjugated to malondialdehyde (MDA)"
 XX
 PN W09842751-A1.
 XX
 PD 01-OCT-1998.
 XX
 PF 20-MAR-1998; 98WO-GB000677.
 XX
 PR 20-MAR-1997; 97GB-00005831.
 XX

PA (UYLE-) UNIV LEICESTER.

PI Lunec J, Bevan R, Griffiths H;

DR WPI; 1999-045137/04.

PT Oxidised fragments of apoprotein B-based low density lipoprotein, LDL -
 PT which inhibits LDL uptake by high affinity LDL receptor, useful e.g. in
 PT treatment and diagnosis of atherosclerosis.
 XX

PS Claim 2; Page 2; 23pp; English.

CC The present sequence is an analogue of apoprotein B 100. The peptide,
 CC which has lys5 conjugated with malondialdehyde (MDA) inhibits uptake of
 CC apoprotein B-based low density lipoprotein (LDL) (or partly modified
 CC forms of LDL) by the high affinity LDL receptor. The peptide and its
 CC analogues are useful in treatment and diagnosis, especially for
 CC atherosclerosis. Atherosclerosis is characterised by thickening and
 CC streaks containing foam cells and, secondly, the formation of fibrous
 CC plaques within the artery. Foam cells are formed by endocytosis of
 CC oxidised LDL by macrophages via a scavenger receptor, which causes cells
 CC to take up more cholesterol than necessary via the high affinity LDL
 CC receptors. The peptides of the invention are oxidised and present
 CC epitopes which prevent oxidised LDL from being taken up by the scavenger
 CC receptor, so preventing LDL uptake by the high affinity LDL receptor, and
 CC possibly preventing foam cell formation
 XX

SO Sequence 11 AA;

Query Match 100.0%; Score 44; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLTRKRGK 9
 |||||
 DB 1 RLTRKRGK 9

RESULT 4
 AAE21732
 ID AAE21732 standard; peptide; 11 AA.

AC AAE21732;
 DT 16-JUL-2002 (first entry)
 DE BSMR effector peptide #2.

XX Bone strength and mineralisation regulatory protein; BSMR; bone strength;
 XX mineralisation; ophthalmological; antidiabetic;
 XX bone density regulating transmembrane receptor; prosthetic device;
 XX surgical implant; diabetic retinopathy; hypertensive retinopathy;
 XX therapy; osteoporosis; prematurity; ocular vessel; eye disorder;
 XX osteopathic.

OS Unidentified.

PN W0200216553-A2.

PD 28-FEB-2002.

PF 17-AUG-2001; 2001WO-US041788.

PR 18-AUG-2000; 2000US-0226119P.

PR 22-SEP-2000; 2000US-0234337P.

PR 13-JUL-2001; 2001US-0304851P.

XX (AVET) AVENTIS PHARMA SA.
 XX (HARD) HARVARD COLLEGE.
 XX (UYCA-) UNIV CASE WESTERN RESERVE.

PI Warman ML, Gong Y, Olsen BR, Rawadi G, Roman-Roman S;

DR WPI; 2002-329694/36.

PT Polynucleotide encoding bone strength and mineralization regulatory
 protein useful for diagnosis or therapy of osteoporosis.

XX Claim 9; Page 78; 124pp; English.

CC The invention relates to bone strength and mineralisation regulatory
 CC protein (BSMR) and its corresponding nucleic acid sequence. BSMR DNA is
 CC useful for the diagnosis or therapy of osteoporosis and for regulating
 CC (increasing) bone strength and mineralisation in a human subject by
 CC activating a bone density regulating transmembrane receptor (BSMR
 CC protein). An expression vector comprising a promoter that is operably
 CC linked to BSMR DNA is useful for modulating bone density and for
 CC enhancing bone strength and mineralisation in a mammal cell. Composition
 CC comprising a BSMR effector is useful for treating osteoporosis and is
 CC useful particularly as a coating for prosthetic devices and surgical
 CC implants. BSMR is useful for screening lead pharmaceutical agents as BSMR
 CC effectors, which may be used to treat a range of eye disorders such as
 CC diabetic retinopathy, hypertensive retinopathy and retinopathy of
 CC prematurity, in which normal vascular growth and integrity of ocular
 CC vessels is disrupted. The present sequence is BSMR effector peptide
 CC XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 44; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLTRKRGK 9
 |||||
 DB 1 RLTRKRGK 9

RESULT 5
 AB007938
 ID AB007938 standard; peptide; 11 AA.

AC AB007938;

DT 23-MAY-2003 (first entry)

DE Apoprotein B 100, residues 3359-3369.

XX Apoprotein B 100; Apo B; human, high affinity low density lipoprotein;
 XX LDL; LDL receptor; immunogen; atherosclerosis; foam cell formation.

OS Homo sapiens.

PN US2002164679-A1.

PD 07-NOV-2002.

PF 20-SEP-1999; 99US-00398902.

PR 20-MAR-1998; 98WO-GB000677.

PA (LUNEC) LUNEC J.
 PA (BEVA/) BEVAN R.
 PA (GRIF/) GRIFFITHS H.

PI Lunec J, Bevan R, Griffiths H;

DR WPI; 2003-328393/31.

PT New molecule useful for diagnosing oxidized low density lipoprotein
 (LDL), and for inhibiting the uptake of LDL by high affinity LDL

PT receptor, or its partially modified form.

XX Claim 1; Page 3; 8pp; English.

XX The invention describes a molecule (I) inhibiting uptake by the high
 CC affinity low density lipoprotein (LDL) receptor of LDL or its partially
 CC modified form. (I) And an antibody (II) that binds (I) are useful in the
 CC manufacture of a medicament for inhibiting uptake by the high affinity
 CC LDL receptor of LDL or a partially modified form of it. (I) And (II) are
 CC useful in the diagnostic test for oxidized LDL, or antibody specific
 CC against oxidized LDL, which will cause uptake by the high affinity LDL
 CC receptor of LDL or a partially modified form of it, by: (a) reacting (I)
 CC or (II) with a sample; (b) detecting an antibody-antigen binding reaction
 CC; and (c) correlating the detection of the antibody-antigen binding
 CC reaction with the presence of oxidized LDL, or antibody specific against
 CC oxidized LDL, which will cause uptake by the high affinity LDL receptor
 CC of LDL or a partially modified form of it. (I) is useful as an immunogen,
 CC e.g., for the production of antibodies, and particularly in the treatment
 CC and diagnosis of atherosclerosis. (I) And (II) are useful as reagents in
 CC diagnostic tests, and for preventing foam cell formation. This is the
 CC amino acid sequence of residues 3359-3369 of Apoprotein B 100 used to
 CC inhibit uptake of the high affinity low density lipoprotein (LDL) by the
 CC LDL receptor
 CC XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 44; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLTRKRGK 9
 |||||
 DB 1 RLTRKRGK 9

RESULT 6
 ADF56451
 ID ADF56451 standard; peptide; 11 AA.

AC ADF564S1,
XX

DT 12-FEB-2004 (first entry)
XX

DE Human apolipoprotein B 100 fragment #2.
XX

KM human; apolipoprotein B 100; malondialdehyde; MDA;
low density lipoprotein; high affinity LDL receptor;
KW high affinity LDL uptake inhibitor; atherosclerosis.

OS Homo sapiens.
XX

PX US2003157567-A1.
PN

PD 21-AUG-2003.
XX

PF 05-FEB-2003; 2003US-00358594.
XX

PR 20-SEP-1999; 99US-00398902.
PA (LUNE/) LUNEC J.
PA (BEVA/) BEVAN R.
PI (GRIF/) GRIFFITHS H.
XX

Lunec J, Bevan R, Griffiths H;
WPI; 2003-697154/66.

New molecule, useful for treating and diagnosing atherosclerosis,
comprises 11 amino acid sequence conjugated with malondialdehyde
inhibits low density lipoprotein receptor.

Claim 2; SEQ ID NO 2; 8bp; English.

The invention relates to a molecule comprising one of three fully defined
amino acid sequences or its partially modified form or analogue, where
lysine is conjugated with malondialdehyde (MDA) and inhibits uptake by
the high affinity low density lipoprotein (LDL) receptor or its partial
modified form. The molecule is useful for treatment or diagnosis of the
human or animal body and in the manufacture of a medicament for
inhibiting uptake by the high affinity LDLR or its partially modified
form. The molecule is useful in a diagnostic test method for antibody
specific against oxidised LDL or oxidised LDL respectively, which will
cause uptake by the high affinity LDLR or its partially modified form.
The molecules and antibodies are for diagnosing and treating
atherosclerosis. The present sequence represents a human apolipoprotein B
100 fragment.

SQ Sequence 11 AA;

Query Match
Best Local Similarity 100.0%; Score 44; DB 7; Length 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLTRKRGALK 9
|||||
||| |
DG 1 RLTRKRGALK 9

RESULT 7
ID AAMw1260
XX AAMw1260 standard; Peptide; 12 AA.
AC AAMw1260;
XX

DI 19-MAY-1998 (first entry)

Apolipoprotein B-100 fragment.

Anxi-coagulant; apolipoprotein B-100; apoB-100; metastatic spread;
thromboplastin-mediated process; cancer; inhibitor; blood coagulation;
KW angiogenesis; cellular differentiation; apoptosis; KRAD-14;
RN prothrombinase complex.

XX	Synthetic.
OS	Homo sapiens.
XX	
PN	M09743311-A1.
XX	
PD	20-NOV-1997.
XX	
PP	09-MAY-1997; 97WO-G8001255.
XX	
PR	09-MAY-1996; 96GB-00009702.
XX	
PA	(UNLO) ROYAL FREE HOSPITAL SCHOOL MED.
XX	
PI	Bruckdorfer KR, Ettelele C;
XX	
DR	WPI; 1998-008798/01.
XX	
PT	Peptide fragments of apo.lipo.protein B-100 with anticoagulant activity used for treating or preventing coagulation, inhibiting angiogenesis,
PT	cell differentiation and apoptosis.
PS	Disclosure: Page 9; 60pp; English.
XX	
CC	This sequence is an example of the peptide of the invention. It has the formula (I), or their variants with one or more internal deletions, CC insertions or substitutions, while retaining anti-coagulant properties, CC apolipoprotein B-100 (apoB-100). Z1-KXO-X1-KKKKRRHS-X2-T-22 (1) X1 = S, Y; X2 = T or I; Z1 = the N terminus of the peptide, or 1-47 amino acids CC (aa); Z2 = the C terminus of the peptide, a terminal amide group or 1-77 CC aa. Compositions containing the peptide, separate or sequential treatment of cancer, particularly brain metastatic spread. They are also used to inhibit thromboplastin-mediated CC processes, specifically to prevent or reduce blood coagulation (e.g., CC during or after surgery or in cases of heart attack, stroke etc.) and to CC inhibit angiogenesis, cellular differentiation or apoptosis. (e.g., CC which is active as such or as part of a 98-aa peptide, RMD-14, CC factor VII on the surface of the prothrombinase complex, and prevents activation of CC it binds to the residues 58-66 of chromoplastin and of platelets by thrombin. CC smaller than apoB-100, they act more quickly
XX	
SQ	Sequence 12 AA;
	Query Match
	Best Local Similarity 100.0%; Score 44; DB 2; Length 12;
	Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 RLTRKGLK 9
	1 RLTRKGLK 9
Db	
RESULT 8	
AAM57207	
ID AAM57207	standard, peptide; 13 AA.
XX	
AC	AAM57207;
XX	
DT	03-AUG-1998 (first entry)
DE	
XX	
APo B 100 binding site peptide analogue peptide B.	
KW	Apo B, binding site; receptor; cancer; drug delivery; anticancer;
KM	growth supplement; non-natural lipid particle; low density lipoprotein;
XX	Ldl, receptor component; apo B100 receptor site.
OS	Synthetic.
XX	
FT	Key Location/Qualifiers
FT	Modified-site 1 /note= "attached to retinoic acid"
XX	

PN WO9813385-A2.
 XX
 PD 02-APR-1998.
 XX
 PF 25-SEP-1997; 97WO-GB002610.
 XX
 PR 27-SEP-1996; 96GB-00020153.
 XX
 PA (UYST) UNIV STRATHCLYDE.
 XX
 PI Halbert GW, Owens MD, Ballie G;
 XX
 DR WPI, 1998-230637/20.
 XX
 PT Non-natural lipid particle comprising peptide binding to apo B protein
 PT receptor - useful as, e.g. vector for delivering drugs to cancer cells
 PT that express this receptor.
 XX
 PS Claim 13; Fig 7; 73pp; English.
 XX
 CC The present sequence represents a specifically claimed Apo B 100 binding
 CC site peptide analogue which can be used as a component of a non-
 CC naturally occurring, receptor-competent low density lipoprotein (LDL)
 CC particle of the present invention. The LDL particle comprises at least 1
 CC peptide component that has at least 1 binding site for an apo B protein
 CC receptor and at least 1 lipophilic substituent. Also described in the
 CC invention are peptides containing an apo B binding sequence with at least
 CC 70% identity with sequences: KAEYKKNKRRH (1) or TRLTRKRGK (2), or their
 CC dimers. Non-naturally occurring, receptor-competent LDL particles are
 CC useful as: (i) drug-targeting vectors for delivering anticancer drugs to
 CC cancer cells that express an apo B protein receptor, and (ii) additives
 CC for cell culture media especially as growth supplements. Non-naturally
 CC occurring, receptor-competent LDL particles do not require the complete
 CC apo B sequence, which is large and tends to aggregate, to provide binding
 CC affinity to an apo B protein receptor
 XX
 SQ Sequence 13 AA;
 XX
 Query Match 100.0%; Score 44; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 RLRKRGK 9
 Db 4 RLRKRGK 12
 XX
 RESULT 9
 AAW22911
 ID AAW22911 standard; peptide; 15 AA.
 XX
 AC AAW22911;
 XX
 DT 02-OCT-1997 (first entry)
 XX
 DE Low density lipoprotein binding peptide.
 XX
 KW Low density; lipoprotein; LDL; binding; absorbent; removal; body fluid;
 KM reagent.
 XX
 OS Synthetic.
 XX
 PN WO9700889-A1.
 XX
 PD 09-JAN-1997.
 XX
 PF 21-JUN-1996; 96WO-JP001734.
 XX
 PR 21-JUN-1995; 95JP-00176904.
 XX
 PA (ASAH) ASAH KASEI KOGYO KK.
 PA (ASAH) ASAH MEDICAL CO LTD.
 XX

PI Hatanaka Y, Aritomi M;
 XX
 DR WPI, 1997-087320/08.
 XX
 PT Peptide binding to low density lipoprotein - useful in removing LDL from
 PT body fluids and as carrier peptide(s) for drugs.
 XX
 PS Example 10; Page 38; 61pp; Japanese.
 XX
 CC The present low density lipoprotein (LDL) binding peptide can be used as
 CC an absorbent to remove LDL from body fluids, or as a LDL binding reagent.
 CC The peptide can be prepared easily and at low cost, and has excellent
 CC stability and preservability. It specifically binds LDL, and does not
 CC cause bradykinin production, white blood cell activation or blood
 CC agglutination
 XX
 SQ Sequence 15 AA;
 XX
 Query Match 100.0%; Score 44; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.12; Length 15;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 RLRKRGK 9
 Db 4 RLRKRGK 12
 XX
 RESULT 10
 AAW41261
 ID AAW41261 standard; peptide; 15 AA.
 XX
 AC AAW41261;
 XX
 DT 19-MAY-1998 (first entry)
 XX
 DE Apolipoprotein B-100 fragment.
 XX
 DE Apolipoprotein B-100 fragment.
 XX
 KM Anti-coagulant; apolipoprotein B-100; apob-100; metastatic spread;
 KM thromboplastin-mediated process; cancer; inhibitor; blood coagulation;
 KM angiogenesis; cellular differentiation; apoptosis; KRAD-14;
 KM prothrombinase complex.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9743311-A1.
 XX
 PD 20-NOV-1997.
 XX
 PF 09-MAY-1997; 97WO-GB001255.
 XX
 PR 09-MAY-1996; 96GB-00009702.
 XX
 PA (UNLO) ROYAL FREE HOSPITAL SCHOOL MED.
 XX
 PI Bruckdorfer KR, Ectrelate C;
 XX
 DR WPI; 1998-008798/01.
 XX
 PT Peptide fragments of apo:lipoprotein B-100 with anticoagulant activity -
 PT used for treating or preventing coagulation, inhibiting angiogenesis,
 PT cell differentiation and apoptosis.
 XX
 PS Disclosure; Page 22; 60pp; English.
 XX
 CC This sequence is an example of the peptide of the invention. It has the
 CC formula (I), or their variants with one or more internal deletions,
 CC insertions or substitutions, while retaining anti-coagulant properties of
 CC apolipoprotein B-100 (apob-100). Z1-KAQ-X1-KKNKRRS-X2-1-22 (I) X1 = S or
 CC Y; X2 = T or I; Z1 = the N terminus of the peptide, or 1-47 amino acids
 CC (aa); Z2 = the C terminus of the peptide, a terminal amide group or 1-77
 CC aa. Compositions containing the peptide are used for simultaneous,
 CC separate or sequential treatment of cancer, particularly to prevent

CC metastatic spread. They are also used to inhibit thromboplastic-mediated
CC processes, specifically to prevent or reduce blood coagulation mediated
CC during or after surgery or in cases of heart failure, stroke, etc., and to
CC inhibit angiogenesis, cellular differentiation or apoptosis (e.g.,
CC activation of the surface of thromboplastin and of platelets by thrombin
CC factor VII on the surface of thromboplastin and of platelets by thrombin
CC it binds to the residues 58-66 of thromboplastin and of platelets by thrombin
CC smaller than apob-100, they act more quickly
SQ Sequence 15 AA;

Query Match
Best Local Similarity 100.0%; Score 44; DB 2; Length 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 RLTNRGKGLK 9
2 RLTNRGKGLK 10

RESULT 11

ID AAM96892 standard; peptide; 15 AA.
XX AAM96892;
AC AAM96892;
XX 22-APR-1999 (first entry)
DE APOB-100 nuclear localisation signal sequence, residues 3353-3367.
XX Human apolipoprotein B-100; apob-100; very-low density lipoprotein; VLDL;
KW apolipoprotein; binding; in vivo transport; nuclear acid; binding domain;
KW non-small cell lung carcinoma; diabetes; arteriosclerosis.
OS Homo sapiens.
PN WO985638-A1.
XX 17-DEC-1998.
PD 10-JUN-1998; 98WO-US011927.
XX 13-JUN-1997; 97US-00874807.
PR 14-MAY-1998; 98US-00079030.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX Guevara JG, Hoogveen RC, Moore JP;
DR WPI; 1999-070331/06.
XX Composition comprising nucleic acid bound to LDL or VLDL lipoprotein -
PT used for delivering nucleic acid to cells for gene therapy and antisense
XX treatment.
XX Claim 19; Fig 13D; 293pp; English.
XX AAM96878-97 represent nuclear localisation signal sequence derived from
CC human apolipoprotein B-100 (apob-100). Apob-100 is a major apoprotein
CC component of very-low density lipoproteins (VLDL); intermediate density
CC lipoprotein (IDL); low density lipoproteins (LDL); and lipoprotein a.
CC The composition describes a composition that comprises the invention. The
CC apolipoprotein describes a composition that comprises the invention. The
CC molecule is used to deliver nucleic acids to eukaryotic cells, in
CC vivo or in vitro, for expressing a therapeutic polypeptide or antisense
CC fibrosis and arteriosclerosis. Specifically they are used for gene therapy of
SQ Sequence 15 AA;

Query Match
Best Local Similarity 100.0%; Score 44; DB 2; Length 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 RLTNRGKGLK 9
7 RLTNRGKGLK 15

RESULT 12

ID ABJ37575 standard; peptide; 20 AA.
XX ABJ37575;
AC ABJ37575;
XX 10-MAY-2003 (first entry)
DE Heparin binding peptide sequence #28.
XX Cytostatic; antirheumatic; antiarthritic; ligand; sulphated; tumour;
KW cardiovascular; circulatory; ligand; sulphated; tumour;
KW rheumatoid arthritis; hypoxia; diabetic retinopathy; heparin.
OS Undifferentiated.
PN WO2003007689-A2.
XX 30-JAN-2003.
PD 22-JUL-2002; 2002WO-US023419.
XX 20-JUL-2001; 2001US-0306726P.
PR (ETHZ-) ETH ZUERICH.
PA (OYU-) UNIV ZURICH.
XX Hubbell JA, Schoenmakers R, Maynard HD;
DR WPI; 2003-300420/29.
XX Use of a ligand comprising of at least one sulfated or sulfonated amino
PT acid for the treatment of e.g. tumors, rheumatoid arthritis, diabetic
XX retinopathy and hypoxia.
XX Disclosure; Fig 2; 79pp; English.
XX The invention relates to a novel ligand for binding a target biomolecule,
CC which comprises a peptide having at least one sulphated or sulfonated amino
CC amino acid and at least one amino acid chosen from neutral and positively
CC charged amino acids. The novel ligands can be used for the treatment of
CC e.g. tumors, rheumatoid arthritis, diabetic retinopathy and hypoxia.
CC This sequence represents a heparin binding peptide relating to the
XX invention
SQ Sequence 20 AA;

Query Match
Best Local Similarity 100.0%; Score 44; DB 6; Length 20;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 RLTNRGKGLK 9
8 RLTNRGKGLK 16

RESULT 13

ID AAM57208 standard; peptide; 22 AA.
XX AAM57208;
AC AAM57208;
XX 03-AUG-1998 (first entry)
DT

```

XX Apo B 100 binding site peptide analogue peptide C.
DE
XX Apo B; binding site; receptor; cancer; drug delivery; anticancer;
KM growth supplement; non-natural lipid particle; low density lipoprotein;
KM LDL; receptor component; apo B100 receptor site.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FT Modified-site 1 /note= "attached to retinoic acid"
FT Modified-site 22 /note= "attached to cholesterol"
FT
XX
XX W09813385-A2.
XX
XX 02-APR-1998.
XX
XX 25-SEP-1997; 97WO-GB002610.
XX
XX 27-SEP-1996; 96GB-00020153.
XX
XX (UYST ) UNIV STRATHCLYDE.
XX
XX Halbert GW, Owens MD, Baillie G;
XX
XX WPI; 1998-230637/20.
XX
XX Non-natural lipid particle comprising peptide binding to apo B protein
PT receptor - useful as, e.g. vector for delivering drugs to cancer cells
PT that express this receptor.
XX
XX Claim 13; Fig 7; 73pp; English.
XX
XX The present sequence represents a specifically claimed Apo B 100 binding
CC site peptide analogue which can be used as a component of a non-
CC naturally occurring, receptor-competent low density lipoprotein (LDL)
CC particle of the present invention. The LDL particle comprises at least 1
CC peptide component that has at least 1 binding site for an apo B protein
CC receptor and at least 1 lipophilic substituent. Also described in the
CC invention are peptides containing an apo B binding sequence with at least
CC 70% identity with sequences: KAEYKKNKGRH (1) or TPTLTRKRGKX (2), or their
CC dimers. Non-naturally occurring, receptor-competent LDL particles are
CC useful as: (i) drug-targeting vectors for delivering anticancer drugs to
CC cancer cells that express an apo B protein receptor, and (ii) additives
CC for cell culture media especially as growth supplements. Non-naturally
CC occurring, receptor-competent LDL particles do not require the complete
CC apo B sequence, which is large and tends to aggregate, to provide binding
CC affinity to an apo B protein receptor
XX
XX
XX Sequence 22 AA:
SQ
Query Match 100.0%; Score 44; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RLTRKRGKX 9
Db 8 RLTRKRGKX 16

```

```

KM growth supplement; non-natural lipid particle; low density lipoprotein;
KM LDL; receptor component; apo B100 receptor site.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FT Modified-site 1 /note= "attached to retinoic acid"
FT Modified-site 22 /note= "attached to cholesterol"
FT
XX
XX W09813385-A2.
XX
XX 02-APR-1998.
XX
XX 25-SEP-1997; 97WO-GB002610.
XX
XX 27-SEP-1996; 96GB-00020153.
XX
XX (UYST ) UNIV STRATHCLYDE.
XX
XX Halbert GW, Owens MD, Baillie G;
XX
XX WPI; 1998-230637/20.
XX
XX Non-natural lipid particle comprising peptide binding to apo B protein
PT receptor - useful as, e.g. vector for delivering drugs to cancer cells
PT that express this receptor.
XX
XX Claim 13; Fig 7; 73pp; English.
XX
XX The present sequence represents a specifically claimed Apo B 100 binding
CC site peptide analogue which can be used as a component of a non-
CC naturally occurring, receptor-competent low density lipoprotein (LDL)
CC particle of the present invention. The LDL particle comprises at least 1
CC peptide component that has at least 1 binding site for an apo B protein
CC receptor and at least 1 lipophilic substituent. Also described in the
CC invention are peptides containing an apo B binding sequence with at least
CC 70% identity with sequences: KAEYKKNKGRH (1) or TPTLTRKRGKX (2), or their
CC dimers. Non-naturally occurring, receptor-competent LDL particles are
CC useful as: (i) drug-targeting vectors for delivering anticancer drugs to
CC cancer cells that express an apo B protein receptor, and (ii) additives
CC for cell culture media especially as growth supplements. Non-naturally
CC occurring, receptor-competent LDL particles do not require the complete
CC apo B sequence, which is large and tends to aggregate, to provide binding
CC affinity to an apo B protein receptor
XX
XX
XX Sequence 22 AA:
SQ
Query Match 100.0%; Score 44; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RLTRKRGKX 9
Db 8 RLTRKRGKX 16

```

```

RESULT 14
AAM57209
ID AAM57209 standard; peptide; 22 AA.
XX
XX AAM57209;
XX
XX 03-AUG-1998 (first entry)
XX
XX Apo B 100 binding site peptide analogue peptide D.
XX
XX Apo B; binding site; receptor; cancer; drug delivery; anticancer;
XX

```

```

RESULT 15
ABR57177
ID ABR57177 standard; peptide; 23 AA.
XX
XX ABR57177;
XX
XX 29-AUG-2003 (first entry)
XX
XX Human PDGFR-beta related navigation peptide SEQ ID NO:25.
XX
XX PDGFR-beta; platelet derived growth factor receptor beta; nanoparticle;
KM delivery; encapsulated molecule; cytostatic; antimicrobial; gene therapy;
KM sustained delivery; cell proliferation disorder; infectious disease;
KM genetic defect; aberrant gene regulation.
XX
XX Homo sapiens.
XX

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2005, 13:14:21 ; Search time 21.1935 Seconds
(without alignments)
28.162 Million cell updates/sec

Title: US-10-657-404A-8
Perfect score: 44
Sequence: 1 RLRKRGK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patente AA: *
1: /cgn2_6/ptodata/1/1aa/5A COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PTCTUS COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfilest.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	10	4	US-09-265-222-20
2	44	100.0	11	4	US-09-265-533A-2
3	44	100.0	11	4	US-09-265-533A-3
4	44	100.0	12	4	US-09-180-422B-13
5	44	100.0	13	4	US-09-265-533A-4
6	44	100.0	15	3	US-08-981-122-85
7	44	100.0	15	4	US-09-180-422B-17
8	44	100.0	15	4	US-09-079-030-205
9	44	100.0	22	4	US-09-265-533A-5
10	44	100.0	22	4	US-09-265-533A-6
11	44	100.0	36	4	US-09-079-030-166
12	44	100.0	51	4	US-09-079-030-98
13	44	100.0	377	1	US-07-959-946-1
14	44	100.0	377	1	US-08-333-577-1
15	44	100.0	377	5	PCT-US92-08634-1
16	44	100.0	420	4	US-09-079-030-223
17	44	100.0	773	4	US-09-079-030-215
18	44	100.0	840	4	US-09-079-030-214
19	44	100.0	4536	4	US-09-180-422B-27
20	44	100.0	4536	4	US-09-079-030-1
21	44	100.0	4563	4	US-09-108-006C-1
22	44	100.0	4563	4	US-09-538-092-842
23	40	90.9	10	4	US-09-265-222-1
24	40	90.9	10	4	US-09-265-222-6
25	39	88.6	10	4	US-09-265-222-5
26	39	88.6	10	4	US-09-265-222-7
27	39	88.6	10	4	US-09-265-222-9

28	39	88.6	10	4	US-09-265-222-11	Sequence 11, Appl
29	39	88.6	10	4	US-09-265-222-12	Sequence 12, Appl
30	38	86.4	10	4	US-09-265-222-2	Sequence 2, Appl1
31	38	86.4	10	4	US-09-265-222-3	Sequence 3, Appl1
32	38	86.4	10	4	US-09-265-222-4	Sequence 4, Appl1
33	38	86.4	785	4	US-09-079-030-216	Sequence 216, App
34	37	84.1	10	4	US-09-265-222-8	Sequence 8, Appl
35	37	84.1	10	4	US-09-265-222-10	Sequence 10, Appl
36	35	79.5	336	4	US-09-489-039A-13630	Sequence 13630, A
37	35	76.1	11	4	US-09-265-222-16	Sequence 16, Appl
38	33.5	76.1	11	4	US-09-265-222-17	Sequence 17, Appl
39	33.5	76.1	11	4	US-09-265-222-18	Sequence 18, Appl
40	33.5	76.1	11	4	US-09-265-222-19	Sequence 19, Appl
41	33	75.0	676	1	US-08-343-785-2	Sequence 2, Appl
42	33	75.0	676	1	US-08-343-785-8	Sequence 8, Appl
43	33	75.0	676	2	US-08-462-221-2	Sequence 2, Appl1
44	33	75.0	676	2	US-08-462-221-8	Sequence 8, Appl1
45	33	75.0	676	3	US-08-946-458-2	Sequence 2, Appl1

ALIGNMENTS

```

RESULT 1
US-09-265-222-20
Sequence 20, Application US/09265222
Patent No. 6579682
GENERAL INFORMATION:
APPLICANT: Innerearity, Thomas
TITLE OF INVENTION: METHODS AND TOOLS FOR IDENTIFYING
TITLE OF INVENTION: COMPOUNDS WHICH MODULATE ATHEROSCLEROSIS BY IMPACTING
FILE REFERENCE: 22002059700
CURRENT FILING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: US/09/265, 222
PRIOR FILING DATE: 1998-03-10
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: BINDING
LOCATION: (1)...(10)
OTHER INFORMATION: Putative proteoglycan binding site of wild-type
OTHER INFORMATION: human apo-B100 protein
US-09-265-222-20

Query Match          100.0%; Score 44; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 RLRKRGK 9
Db      2 RLRKRGK 10

RESULT 2
US-09-265-533A-2
Sequence 2, Application US/0926533A
Patent No. 6670452
GENERAL INFORMATION:
APPLICANT: University of Strathclyde
APPLICANT: Owens, Moira
APPLICANT: Ballie, George
TITLE OF INVENTION: NO. 6670452-Naturally Occurring Lipoprotein Particle
FILE REFERENCE: P078655
CURRENT APPLICATION NUMBER: US/09/269, 533A
CURRENT FILING DATE: 1999-06-01

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;; PRIOR APPLICATION NUMBER: PCT/GB97/02610
;; PRIOR FILING DATE: 1997-09-25
;; PRIOR APPLICATION NUMBER: GB 9620153.8
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: Patentin version 3.0
;; SEQ ID NO: 2
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1..1)
;; OTHER INFORMATION: Apo B binding site sequence
US-09-269-533A-2

Query Match
Best Local Similarity 100.0%; Score 44; DB 4; Length 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RLRKRGK 9
Db 3 RLRKRGK 11

RESULT 3
US-09-269-533A-3
;; Sequence 3, Application US/09269533A
;; Patent No. 6670452
;; GENERAL INFORMATION:
;; APPLICANT: University of Strathclyde
;; APPLICANT: Halbert, Gavin
;; APPLICANT: Owens, Moira
;; TITLE OF INVENTION: No. 6670452-Naturally Occurring Lipoprotein Particle
;; FILE REFERENCE: P07885US
;; CURRENT APPLICATION NUMBER: US/09/269,533A
;; PRIOR FILING DATE: 1999-06-01
;; PRIOR APPLICATION NUMBER: PCT/GB97/02610
;; PRIOR FILING DATE: 1997-09-25
;; PRIOR APPLICATION NUMBER: GB 9620153.8
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: Patentin version 3.0
;; SEQ ID NO: 3
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1..1)
;; OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site
;; NAME/KEY: misc_feature
;; LOCATION: (1..1)
;; OTHER INFORMATION: Cholesterol linked at C-terminus of peptide analogue
US-09-269-533A-3

Query Match
Best Local Similarity 100.0%; Score 44; DB 4; Length 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RLRKRGK 9
Db 2 RLRKRGK 10

RESULT 4
US-09-180-422B-13
;; Sequence 13, Application US/09180422B
;; Patent No. 644644

;; GENERAL INFORMATION:
;; APPLICANT: BRUCKDORFER, KARL R
;; ETTLELAIE, CAMILLE
;; TITLE OF INVENTION: ANTICOAGULANT PEPTIDE FRAGMENTS DERIVED
;; FROM APOBOLIPROTEIN B-100
;; NUMBER OF SEQUENCES: 27
;; CORRESPONDENCE ADDRESS:
;; ADDRESSER: NIXON & VANDERHAYE, P. C.
;; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
;; CITY: ARLINGTON
;; STATE: VA
;; COUNTRY: USA
;; ZIP: 22201
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/180,422B
;; FILING DATE: 07-Dec-1998
;; CLASSIFICATION: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: SADOFF, B. J.
;; REGISTRATION NUMBER: 36663
;; REFERENCE/DOCKET NUMBER: 117-268
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 7038164000
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-180-422B-13

Query Match
Best Local Similarity 100.0%; Score 44; DB 4; Length 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RLRKRGK 9
Db 1 RLRKRGK 9

RESULT 5
US-09-269-533A-4
;; Sequence 4, Application US/09269533A
;; Patent No. 6670452
;; GENERAL INFORMATION:
;; APPLICANT: University of Strathclyde
;; APPLICANT: Halbert, Gavin
;; APPLICANT: Owens, Moira
;; TITLE OF INVENTION: No. 6670452-Naturally Occurring Lipoprotein Particle
;; FILE REFERENCE: P07885US
;; CURRENT APPLICATION NUMBER: US/09/269,533A
;; PRIOR FILING DATE: 1999-06-01
;; PRIOR APPLICATION NUMBER: PCT/GB97/02610
;; PRIOR FILING DATE: 1997-09-25
;; PRIOR APPLICATION NUMBER: GB 9620153.8
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: Patentin version 3.0
;; SEQ ID NO: 4
;; LENGTH: 13
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; NAME/KEY: misc_feature

LOCATION: ()
 OTHER INFORMATION: Synthesized peptide analogue of the Apo B 100 binding site
 NAME/KEY: misc:feature
 LOCATION: ()
 OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue
 US-09-269-533A-4

Query Match 100.0%; Score 44; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.034;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLRKRGK 9
 |||||
 Db 4 RLRKRGK 12

RESULT 6
 US-08-981-122-85
 Sequence 85, Application US/08981122B
 Patent No. 6127339
 GENERAL INFORMATION:
 APPLICANT: Hatanaka, Yoshihiro
 APPLICANT: Aritomi, Masaharu
 TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
 FILE REFERENCE:
 CURRENT APPLICATION NUMBER: US/08/981,122B
 CURRENT FILING DATE: 1997-12-18
 PRIOR APPLICATION NUMBER: JP 7-176904
 PRIOR FILING DATE: 1995-06-21
 PRIOR APPLICATION NUMBER: PCT/JP96/01734
 PRIOR FILING DATE: 1996-06-21
 NUMBER OF SEQ ID NOS: 90
 SOFTWARE: Patent Ver. 2.0
 SEQ ID NO 85
 LENGTH: 15
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Sequence of a peptide synthesized in Comparative Example 7 from
 Patent No. 6127339
 OTHER INFORMATION: L-form F-moc amino acids by solid phase method using an
 OTHER INFORMATION: automatic peptide synthesizer (9050 plus peptide synthesizer)
 PUBLICATION INFORMATION:
 AUTHORS: Urban Olsson et al.
 TITLE: Binding of a synthetic apolipoprotein B-100 peptide and peptide
 TITLE: analogues to chondroitin 6-sulfate: Effects of the lipid environment
 JOURNAL: Biochemistry
 VOLUME: 32
 PAGES: 1858-1865
 US-08-981-122-85

Query Match 100.0%; Score 44; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.039;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLRKRGK 9
 |||||
 Db 4 RLRKRGK 12

RESULT 7
 US-09-180-422B-17
 Sequence 17, Application US/09180422B
 Patent No. 6444644
 GENERAL INFORMATION:
 APPLICANT: BRUCKDORFER, KARL R
 ETTELAIE, CAMILLE
 TITLE OF INVENTION: ANTICOAGULANT PEPTIDE FRAGMENTS DERIVED
 FROM APOLOPROTEIN B-100
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHAY, P.C.
 STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR

CITY: ARLINGTON
 STATE: VA
 COUNTRY: USA
 ZIP: 22201
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/180,422B
 FILING DATE: 07-Dec-1998
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: SADOFF, B.J.
 REGISTRATION NUMBER: 36663
 REFERENCE/DOCKET NUMBER: 117-268
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 7038164000
 TELEFAX: 7038164100
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 17:
 US-09-180-422B-17

Query Match 100.0%; Score 44; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.039;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLRKRGK 9
 |||||
 Db 2 RLRKRGK 10

RESULT 8
 US-09-079-030-205
 Sequence 205, Application US/09079030
 Patent No. 6635623
 GENERAL INFORMATION:
 APPLICANT: Guevera, Jr., Juan G.
 APPLICANT: Hoogeveen, Ron C.
 APPLICANT: Moore, Paul J.
 TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
 TITLE OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
 NUMBER OF SEQUENCES: 229
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: USA
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/079,030
 FILING DATE: Concurrently Herewith
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: McMillian, Nabesla R.
 REGISTRATION NUMBER: P-43,363
 REFERENCE/DOCKET NUMBER: ARAG:003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577

; INFORMATION FOR SEQ ID NO: 205:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-079-030-205

Query Match
Best Local Similarity 100.0%; Score 44; DB 4; Length 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLTRRGGLK 9
Db 7 RLTRRGGLK 15

RESULT 9
US-09-269-533A-5
; Sequence 5, Application US/09269533A
; Patent No. 6670452
; GENERAL INFORMATION:
; APPLICANT: University of Strathclyde
; APPLICANT: Halbert, Gavin
; APPLICANT: Owens, Moira
; APPLICANT: Baillie, George
; TITLE OF INVENTION: No. 6670452-Naturally Occurring Lipoprotein Particle
; FILE REFERENCE: P07885US
; CURRENT APPLICATION NUMBER: US/09/269,533A
; CURRENT FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: PCT/GB97/02610
; PRIOR FILING DATE: 1997-09-25
; PRIOR APPLICATION NUMBER: GB 9620153.8
; PRIOR FILING DATE: 1996-09-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site
; NAME/KEY: misc.feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Cholesterol linked at C-terminus of peptide analogue
; NAME/KEY: misc.feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue
US-09-269-533A-5

Query Match
Best Local Similarity 100.0%; Score 44; DB 4; Length 22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLTRRGGLK 9
Db 8 RLTRRGGLK 16

RESULT 10
US-09-269-533A-6
; Sequence 6, Application US/09269533A
; Patent No. 6670452
; GENERAL INFORMATION:
; APPLICANT: University of Strathclyde
; APPLICANT: Halbert, Gavin
; APPLICANT: Owens, Moira
; APPLICANT: Baillie, George
; TITLE OF INVENTION: No. 6670452-Naturally Occurring Lipoprotein Particle
; FILE REFERENCE: P07885US
; CURRENT APPLICATION NUMBER: US/09/269,533A

; CURRENT FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: PCT/GB97/02610
; PRIOR FILING DATE: 1997-09-25
; PRIOR APPLICATION NUMBER: GB 9620153.8
; PRIOR FILING DATE: 1996-09-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site
; NAME/KEY: misc.feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue
US-09-269-533A-6

Query Match
Best Local Similarity 100.0%; Score 44; DB 4; Length 22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLTRRGGLK 9
Db 8 RLTRRGGLK 16

RESULT 11
US-09-079-030-166
; Sequence 166, Application US/09079030
; Patent No. 6635623
; GENERAL INFORMATION:
; APPLICANT: Guevara, Jr., Juan G.
; APPLICANT: Hoogewegen, Ron C.
; APPLICANT: Moore, Paul J.
; TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
; NUMBER OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
; NUMBER OF SEQUENCES: 229
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,030
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMillian, Nabesla R.
; REGISTRATION NUMBER: P-43,363
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 166:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-079-030-166

Query Match
Best Local Similarity 100.0%; Score 44; DB 4; Length 36;
Matches 100.0%; Pred. No. 0.089;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLTRRGGLK 9
| | | | |
DB 12 RLTRRGGLK 20

RESULT 12

US-09-079-030-98
Sequence 98, Application US/09079030
Patent No. 6635623
GENERAL INFORMATION:
APPLICANT: Guevera, Jr., Juan G.
APPLICANT: Hoozeveen, Ron C.
APPLICANT: Moore, Paul J.
TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
NUMBER OF SEQUENCES: 229
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,030
FILING DATE: Concurrently Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMillian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: ABAG:003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-079-030-98

Query Match 100.0%; Score 44; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLTRRGGLK 9
| | | | |
DB 7 RLTRRGGLK 15

RESULT 13
US-07-959-946-1
Sequence 1, Application US/07959946
Patent No. 5408038
GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Witzum, Joseph L.
APPLICANT: Curtiss, Linda K.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Shore, Sutter &

ADDRESSEE: Milnamow, Ltd.
STREET: 180 No. 5408038th Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,946
FILING DATE: 19921008
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,706
FILING DATE: 18-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5460
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 377 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-959-946-1

Query Match 100.0%; Score 44; DB 1; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLTRRGGLK 9
| | | | |
DB 146 RLTRRGGLK 154

RESULT 14
US-08-333-577-1
Sequence 1, Application US/08333577
Patent No. 5786206
GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Witzum, Joseph L.
APPLICANT: Curtiss, Linda K.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Shore, Sutter &
STREET: 180 No. 5786206th Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,577
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:

NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: SCRF 234.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 377 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-333-577-1

Query Match 100.0%; Score 44; DB 1; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RLTRRRGLK 9
|||
Db 146 RLTRRRGLK 154

RESULT 15

PCT-US92-08634-1
Sequence 1, Application PC/TUS9208634
GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Wiltum, Joseph L.
APPLICANT: Curtiss, Linda K.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
ADDRESSEE: Milnamow, Ltd.
STREET: 180 North Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08634
FILING DATE: 19921009
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,706
FILING DATE: 18-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 377 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-08634-1

Query Match 100.0%; Score 44; DB 5; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RLTRRRGLK 9
|||
Db 146 RLTRRRGLK 154

Search completed: January 12, 2005, 13:33:16
Job time : 21.1935 secs

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OM protein - protein search, using sw model

Run on: January 12, 2005, 13:31:02 ; Search time 72.2903 Seconds

(without alignments)
44.980 Million cell updates/sec

Title: US-10-657-404A-8

Perfect score: 44

Sequence: 1 RLTRKRGK 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :	Published Applications AA:*
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11:	/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12:	/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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17:	/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18:	/cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19:	/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	9	17	US-10-657-404A-8
2	44	100.0	10	9	US-09-823-418-20
3	44	100.0	10	9	US-09-822-965-20
4	44	100.0	11	9	US-09-269-533A-2
5	44	100.0	11	9	US-09-269-533A-3
6	44	100.0	11	9	US-09-398-902-2
7	44	100.0	11	14	US-09-931-375A-76
8	44	100.0	11	14	US-10-358-594-2
9	44	100.0	11	17	US-10-657-404A-2
10	44	100.0	11	17	US-10-657-404A-3
11	44	100.0	13	9	US-09-269-533A-4
12	44	100.0	13	17	US-10-657-404A-4
13	44	100.0	22	9	US-09-269-533A-5

14	44	100.0	22	9	US-09-269-533A-6	Sequence 6, Appli
15	44	100.0	22	17	US-10-657-404A-5	Sequence 5, Appli
16	44	100.0	22	17	US-10-657-404A-6	Sequence 6, Appli
17	44	100.0	25	17	US-10-657-404A-9	Sequence 9, Appli
18	44	100.0	34	15	US-10-333-113-1	Sequence 1, Appli
19	44	100.0	34	9	US-09-864-761-46837	Sequence 46837, A
20	44	100.0	3000	16	US-10-741-601-431	Sequence 431, App
21	44	100.0	4563	9	US-09-870-759-128	Sequence 128, App
22	44	100.0	4563	10	US-09-802-640-32	Sequence 32, App
23	44	100.0	4563	10	US-09-751-708A-128	Sequence 128, App
24	44	100.0	4563	14	US-10-403-902A-32	Sequence 32, Appli
25	44	100.0	4563	16	US-10-741-601-432	Sequence 432, App
26	44	100.0	4563	16	US-10-741-601-433	Sequence 433, App
27	44	100.0	4563	17	US-10-428-877A-124	Sequence 124, App
28	40	90.9	10	9	US-09-823-418-1	Sequence 1, Appli
29	40	90.9	10	9	US-09-823-418-6	Sequence 6, Appli
30	40	90.9	10	9	US-09-822-965-1	Sequence 1, Appli
31	40	90.9	10	9	US-09-822-965-6	Sequence 6, Appli
32	39	88.6	10	9	US-09-823-418-5	Sequence 5, Appli
33	39	88.6	10	9	US-09-823-418-7	Sequence 7, Appli
34	39	88.6	10	9	US-09-823-418-9	Sequence 9, Appli
35	39	88.6	10	9	US-09-823-418-11	Sequence 11, Appli
36	39	88.6	10	9	US-09-823-418-12	Sequence 12, Appli
37	39	88.6	10	9	US-09-823-965-5	Sequence 5, Appli
38	39	88.6	10	9	US-09-822-965-7	Sequence 7, Appli
39	39	88.6	10	9	US-09-822-965-9	Sequence 9, Appli
40	39	88.6	10	9	US-09-822-965-11	Sequence 11, Appli
41	39	88.6	10	9	US-09-822-965-12	Sequence 12, Appli
42	38	86.4	10	9	US-09-823-418-2	Sequence 2, Appli
43	38	86.4	10	9	US-09-823-418-3	Sequence 3, Appli
44	38	86.4	10	9	US-09-823-418-4	Sequence 4, Appli
45	38	86.4	10	9	US-09-822-965-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-657-404A-8
; Sequence 8, Application US/10657404A
; Publication No. US20040235730A1
; GENERAL INFORMATION:
; APPLICANT: University of Strathclyde
; APPLICANT: Halbert, Gavin
; APPLICANT: Owens, Moira
; TITLE OF INVENTION: Non-Naturally Occurring Lipoprotein Particle
; FILE REFERENCE: P07885US-CIP
; CURRENT APPLICATION NUMBER: US/10/657,404A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: PCT/GB97/02610
; PRIOR FILING DATE: 1997-09-25
; PRIOR APPLICATION NUMBER: GB 9620153.8
; PRIOR FILING DATE: 1996-09-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Apo B binding site sequence
US-10-657-404A-8

Query Match 100.0%; Score 44; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY 1 RLTRKRGK 9
|||
DB 1 RLTRKRGK 9

RESULT 2
US-09-823-418-20
; Sequence 20, Application US/09823418
; Publication No. US20010024797A1
; GENERAL INFORMATION:
; APPLICANT: Innervital, Thomas
; APPLICANT: Innervital, Thomas
; TITLE OF INVENTION: METHODS AND TOOLS FOR IDENTIFYING COMPOUNDS
; TITLE OF INVENTION: WHICH MODULATE ATHEROSCLEROSIS BY IMPACTING
; FILE REFERENCE: 220002059711
; CURRENT APPLICATION NUMBER: US/09/823,418
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: US 09/265,222
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: US 60/077,618
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)...(10)
; OTHER INFORMATION: Putative proteoglycan binding site of wild-type
US-09-823-418-20

Query Match
Best Local Similarity 100.0%; Score 44; DB 9; Length 10;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RLTRKRGK 9
Db 2 RLTRKRGK 10

RESULT 3
US-09-822-965-20
; Sequence 20, Application US/09822965
; Publication No. US20010029027A1
; GENERAL INFORMATION:
; APPLICANT: Innervital, Thomas
; APPLICANT: Innervital, Thomas
; TITLE OF INVENTION: METHODS AND TOOLS FOR IDENTIFYING
; TITLE OF INVENTION: COMPOUNDS WHICH MODULATE ATHEROSCLEROSIS BY IMPACTING
; FILE REFERENCE: 220002059710
; CURRENT APPLICATION NUMBER: US/09/822,965
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: US 09/265,222
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: US 60/077,618
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)...(10)
; OTHER INFORMATION: Putative proteoglycan binding site of wild-type
US-09-822-965-20

Query Match
Best Local Similarity 100.0%; Score 44; DB 9; Length 10;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLTRKRGK 9
Db 2 RLTRKRGK 10

RESULT 4
US-09-269-533A-2
; Sequence 2, Application US/09269533A
; Patent No. US20020147304A1
; GENERAL INFORMATION:
; APPLICANT: University of Strathclyde
; APPLICANT: Halbert, Gavin
; APPLICANT: Owens, Moira
; TITLE OF INVENTION: No. US20020147304A1-Naturally Occurring Lipoprotein Particle
; FILE REFERENCE: P0788505
; CURRENT APPLICATION NUMBER: US/09/269,533A
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: PCT/GB97/02610
; PRIOR FILING DATE: 1997-09-25
; PRIOR APPLICATION NUMBER: GB 9620153.8
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(7)
; OTHER INFORMATION: Apo B binding site sequence
US-09-269-533A-2

Query Match
Best Local Similarity 100.0%; Score 44; DB 9; Length 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RLTRKRGK 9
Db 3 RLTRKRGK 11

RESULT 5
US-09-269-533A-3
; Sequence 3, Application US/09269533A
; Patent No. US20020147304A1
; GENERAL INFORMATION:
; APPLICANT: University of Strathclyde
; APPLICANT: Halbert, Gavin
; APPLICANT: Owens, Moira
; TITLE OF INVENTION: No. US20020147304A1-Naturally Occurring Lipoprotein Particle
; FILE REFERENCE: P0788505
; CURRENT APPLICATION NUMBER: US/09/269,533A
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: PCT/GB97/02610
; PRIOR FILING DATE: 1997-09-25
; PRIOR APPLICATION NUMBER: GB 9620153.8
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(7)
; OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site
LOCATION: (1)...(7)
; OTHER INFORMATION: Cholesterol linked at C-terminus of peptide analogue

Query Match
Best Local Similarity 100.0%; Score 44; DB 9; Length 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

NAME/KEY: misc feature
LOCATION: ()
OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue
US-09-269-533A-3

Query Match
Best Local Similarity 100.0%; Score 44; DB 9; Length 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLTRRGGLK 9
Db 2 RLTRRGGLK 10

RESULT 6
US-09-398-902-2
Sequence 2, Application US/09398902
Patent No. US20020164679A1
GENERAL INFORMATION:
APPLICANT: Lunec, Joe
APPLICANT: Bevan, Ruth
APPLICANT: Griffiths, Helen
TITLE OF INVENTION: OXIDISED FRAGMENTS OF APOLIPOPROTEIN B AND THEIR USE
FILE REFERENCE: 3523P003
CURRENT APPLICATION NUMBER: US/09/398,902
CURRENT FILING DATE: 1999-09-20
PRIOR APPLICATION NUMBER: PCT/GB98/00677
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: GB 9705831.7
PRIOR FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-09-398-902-2

Query Match
Best Local Similarity 100.0%; Score 44; DB 9; Length 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLTRRGGLK 9
Db 1 RLTRRGGLK 9

RESULT 7
US-09-931-375A-76
Sequence 76, Application US/09931375A
Publication No. US20030027151A1
GENERAL INFORMATION:
APPLICANT: WARMAN, Matthew L.
APPLICANT: GONG, Yaodan
APPLICANT: OLSEN, Bjorn R.
APPLICANT: RAWADI, Georges
APPLICANT: ROMAN-ROMAN, Sergiu
TITLE OF INVENTION: REGULATOR GENE AND SYSTEM USEFUL FOR THE DIAGNOSIS AND THERAPY OF
FILE REFERENCE: 38464-0004
CURRENT APPLICATION NUMBER: US/09/931,375A
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 60/304,851
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/234,337
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 60/226,119
PRIOR FILING DATE: 2000-08-18
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.0
SEQ ID NO 76
LENGTH: 11
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide that can act as an effector of BSMR
US-09-931-375A-76

Query Match
Best Local Similarity 100.0%; Score 44; DB 10; Length 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLTRRGGLK 9
Db 1 RLTRRGGLK 9

RESULT 8
US-10-358-594-2
Sequence 2, Application US/10358594
Publication No. US20030157567A1
GENERAL INFORMATION:
APPLICANT: Lunec, Joe
APPLICANT: Bevan, Ruth
APPLICANT: Griffiths, Helen
TITLE OF INVENTION: OXIDISED FRAGMENTS OF APOLIPOPROTEIN B AND THEIR USE
FILE REFERENCE: 3523P003
CURRENT APPLICATION NUMBER: US/10/358,594
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/398,902
PRIOR FILING DATE: 1999-09-20
PRIOR APPLICATION NUMBER: PCT/GB98/00677
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: GB 9705831.7
PRIOR FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-10-358-594-2

Query Match
Best Local Similarity 100.0%; Score 44; DB 14; Length 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLTRRGGLK 9
Db 1 RLTRRGGLK 9

RESULT 9
US-10-657-404A-2
Sequence 2, Application US/10657404A
Publication No. US20040235730A1
GENERAL INFORMATION:
APPLICANT: University of Strathclyde
APPLICANT: Halbert, Gavin
APPLICANT: Owens, Molra
APPLICANT: Baillie, George
TITLE OF INVENTION: Non-Naturally Occurring Lipoprotein Particle
FILE REFERENCE: P07865US-CIP
CURRENT APPLICATION NUMBER: US/10/657,404A
CURRENT FILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: PCT/GB97/02610
PRIOR FILING DATE: 1997-09-25
PRIOR APPLICATION NUMBER: GB 9620153.8
PRIOR FILING DATE: 1996-09-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

/ NAME/KEY: misc feature
/ OTHER INFORMATION: Apo B binding site sequence
US-10-657-404a-2

Query Match 100.0%; Score 44; DB 17; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLTRKRGK 9
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Db 3 RLTRKRGK 11

RESULT 10
US-10-657-404a-3
/ Sequence 3, Application US/10657404A
/ Publication No. US20040235730A1
/ GENERAL INFORMATION:
/ APPLICANT: University of Strathclyde
/ APPLICANT: Halbert, Gavin
/ APPLICANT: Owens, Moira
/ APPLICANT: Baillie, George
/ TITLE OF INVENTION: Non-Naturally Occurring Lipoprotein Particle
/ FILE REFERENCE: P07885US-CIP
/ CURRENT APPLICATION NUMBER: US/10/657,404A
/ PRIOR FILING DATE: 2003-09-08
/ PRIOR APPLICATION NUMBER: PCT/GB97/02610
/ PRIOR FILING DATE: 1997-09-25
/ PRIOR APPLICATION NUMBER: GB 9620153.8
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Cholesterol linked at C-terminus of peptide analogue
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue
US-10-657-404a-3

Query Match 100.0%; Score 44; DB 17; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLTRKRGK 9
| | | | | | | | | |
Db 2 RLTRKRGK 10

RESULT 11
US-09-269-533a-4
/ Sequence 4, Application US/09269533A
/ Patent No. US20020147304A1
/ GENERAL INFORMATION:
/ APPLICANT: University of Strathclyde
/ APPLICANT: Halbert, Gavin
/ APPLICANT: Owens, Moira
/ APPLICANT: Baillie, George
/ TITLE OF INVENTION: No. US20020147304A1-Naturally Occurring Lipoprotein Particle
/ FILE REFERENCE: P07885US
/ CURRENT APPLICATION NUMBER: US/09/269,533A
/ PRIOR FILING DATE: 1999-06-01
/ PRIOR APPLICATION NUMBER: PCT/GB97/02610
/ PRIOR FILING DATE: 1997-09-25
/ PRIOR APPLICATION NUMBER: GB 9620153.8
/ PRIOR FILING DATE: 1996-09-27

/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 4
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: ()..()
/ OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site
/ NAME/KEY: misc feature
/ LOCATION: ()..()
/ OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue
US-09-269-533a-4

Query Match 100.0%; Score 44; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLTRKRGK 9
| | | | | | | | | |
Db 4 RLTRKRGK 12

RESULT 12
US-10-657-404a-4
/ Sequence 4, Application US/10657404A
/ Publication No. US20040235730A1
/ GENERAL INFORMATION:
/ APPLICANT: University of Strathclyde
/ APPLICANT: Halbert, Gavin
/ APPLICANT: Owens, Moira
/ APPLICANT: Baillie, George
/ TITLE OF INVENTION: Non-Naturally Occurring Lipoprotein Particle
/ FILE REFERENCE: P07885US-CIP
/ CURRENT APPLICATION NUMBER: US/10/657,404A
/ PRIOR FILING DATE: 2003-09-08
/ PRIOR APPLICATION NUMBER: PCT/GB97/02610
/ PRIOR FILING DATE: 1997-09-25
/ PRIOR APPLICATION NUMBER: GB 9620153.8
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 4
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue
US-10-657-404a-4

Query Match 100.0%; Score 44; DB 17; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLTRKRGK 9
| | | | | | | | | |
Db 4 RLTRKRGK 12

RESULT 13
US-09-269-533a-5
/ Sequence 5, Application US/09269533A
/ Patent No. US20020147304A1
/ GENERAL INFORMATION:
/ APPLICANT: University of Strathclyde
/ APPLICANT: Halbert, Gavin
/ APPLICANT: Owens, Moira
/ APPLICANT: Baillie, George

TITLE OF INVENTION: No. US20020147304A1-Naturally Occurring Lipoprotein Particle
 FILE REFERENCE: P07885US
 CURRENT APPLICATION NUMBER: US/09/269,533A
 CURRENT FILING DATE: 1998-06-01
 PRIOR APPLICATION NUMBER: PCT/GB97/02610
 PRIOR FILING DATE: 1997-09-25
 PRIOR APPLICATION NUMBER: GB 9620153.8
 PRIOR FILING DATE: 1996-09-27
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 5
 LENGTH: 22
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1..7)
 OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site
 NAME/KEY: misc feature
 LOCATION: (1..7)
 OTHER INFORMATION: Cholesterol linked at C-terminus of peptide analogue
 NAME/KEY: misc feature
 LOCATION: (1..1)
 OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue
 US-09-269-533A-5

Query Match 100.0%; Score 44; DB 9; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RLTRRGGLK 9
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 Db 8 RLTRRGGLK 16

RESULT 14
 US-09-269-533A-6
 Sequence 6, Application US/09269533A
 Patent No. US20020147304A1
 GENERAL INFORMATION:
 APPLICANT: University of Strathclyde
 APPLICANT: Halbert, Gavin
 APPLICANT: Owens, Molra
 APPLICANT: Baillie, George
 TITLE OF INVENTION: No. US20020147304A1-Naturally Occurring Lipoprotein Particle
 FILE REFERENCE: P07885US
 CURRENT APPLICATION NUMBER: US/09/269,533A
 CURRENT FILING DATE: 1999-06-01
 PRIOR APPLICATION NUMBER: PCT/GB97/02610
 PRIOR FILING DATE: 1997-09-25
 PRIOR APPLICATION NUMBER: GB 9620153.8
 PRIOR FILING DATE: 1996-09-27
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 6
 LENGTH: 22
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1..7)
 OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site
 NAME/KEY: misc feature
 LOCATION: (1..1)
 OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue
 US-09-269-533A-6

Query Match 100.0%; Score 44; DB 9; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RLTRRGGLK 9
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Db 8 RLTRRGGLK 16

RESULT 15
 US-10-657-404A-5
 Sequence 5, Application US/10657404A
 Publication No. US20040235730A1
 GENERAL INFORMATION:
 APPLICANT: University of Strathclyde
 APPLICANT: Halbert, Gavin
 APPLICANT: Owens, Molra
 APPLICANT: Baillie, George
 TITLE OF INVENTION: Non-Naturally Occurring Lipoprotein Particle
 FILE REFERENCE: P07885US-CIP
 CURRENT APPLICATION NUMBER: US/10/657,404A
 CURRENT FILING DATE: 2003-09-08
 PRIOR APPLICATION NUMBER: PCT/GB97/02610
 PRIOR FILING DATE: 1997-09-25
 PRIOR APPLICATION NUMBER: GB 9620153.8
 PRIOR FILING DATE: 1996-09-27
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 5
 LENGTH: 22
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1..7)
 OTHER INFORMATION: Synthesised peptide analogue of the Apo B 100 binding site
 NAME/KEY: misc feature
 LOCATION: (1..7)
 OTHER INFORMATION: Cholesterol linked at C-terminus of peptide analogue
 NAME/KEY: misc feature
 LOCATION: (1..1)
 OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue
 US-10-657-404A-5

Query Match 100.0%; Score 44; DB 17; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RLTRRGGLK 9
 |||||
 Db 8 RLTRRGGLK 16

Search completed: January 12, 2005, 13:52:50
 Job time : 72.2903 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 12, 2005, 13:13:31 ; Search time 16.5484 Seconds
(without alignments)
52.328 Million cell updates/sec

Title: US-10-657-404A-8
Perfect score: 44
Sequence: 1 RLTRKRGK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	269	2 C60950	apolipoprotein B-1
2	44	100.0	596	2 S32802	apolipoprotein B -
3	44	100.0	779	2 JH0102	apolipoprotein B -
4	44	100.0	4563	1 LPHUB	apolipoprotein B-1
5	39	88.6	274	2 A60950	apolipoprotein B-1
6	39	88.6	275	2 E60950	apolipoprotein B-1
7	38	86.4	784	2 JH0101	apolipoprotein B-1
8	37	84.1	680	2 A81875	apolipoprotein B-1
9	35	79.5	305	2 A75334	hypothetical prote
10	34	77.3	561	1 S34191	lacyl-carrier-proc
11	33	75.0	107	2 S32607	sulfite reductase
12	33	75.0	112	2 S33822	salivary glue prot
13	33	75.0	198	2 T41529	salivary glue prot
14	33	75.0	259	1 B69407	hypothetical prote
15	33	75.0	309	2 AH0906	Mj0188 homolog - A
16	33	75.0	401	2 E75213	conserved hypoch
17	33	75.0	676	2 A40363	nife protein PAB01
18	33	75.0	1058	2 S65460	DNA ligase (NAD)
19	33	75.0	1778	2 JH0382	apolipoprotein B -
20	33	75.0	2629	2 I46569	apolipoprotein B -
21	32	72.7	188	2 F87217	conserved hypoch
22	32	72.7	197	2 JH4150	ribosomal protein
23	32	72.7	219	2 A53305	pentose-5-phosphat
24	32	72.7	258	2 T01873	hypothetical prote
25	32	72.7	330	1 F69534	pyruvate formate-1
26	32	72.7	339	1 F82654	phage-related inte
27	32	72.7	363	1 A29376	cellular tumor ant
28	32	72.7	436	2 F64466	protein F2839.3 [i
29	32	72.7	668	1 S74619	hypothetical prote

30	32	72.7	1073	2 T01955	hypothetical prote
31	32	72.7	1241	2 H84486	probable helicase
32	32	72.7	1265	2 F84517	probable helicase
33	32	72.7	1678	2 D6481	189.6K hypothetical
34	32	72.7	1752	2 T48965	hypothetical prote
35	31	70.5	84	2 G87376	hypothetical prote
36	31	70.5	168	2 T03168	hypothetical prote
37	31	70.5	228	2 TMMUG1	trichome different
38	31	70.5	232	1 S28609	phosphoadenylyl-su
39	31	70.5	249	2 B82400	tonal protein VCA0
40	31	70.5	290	2 S39854	crax protein - Str
41	31	70.5	304	2 A98146	probable threonin
42	31	70.5	309	1 E65112	hypothetical 34.6
43	31	70.5	309	2 E85985	hypothetical prote
44	31	70.5	309	2 B91140	hypothetical prote
45	31	70.5	336	2 AC3142	threonine dehydrat

ALIGNMENTS

RESULT 1

C60950
apolipoprotein B-100 - golden hamster (fragment)
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: C60950
R:Law, A.; Scott, J.
J. Lipid Res. 31, 1109-1120, 1990
A:Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL
A:Reference number: A60950, MUID:90324804, PMID:2373961
A:Accession: C60950
A:Molecule type: DNA
A:Residues: 1-269 <LAW>
A:Cross-references: UNIPROT:Q60537; UNIPROT:Q60536
C:Superfamily: apolipoprotein B
C:Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;

Query Match 100.0%; Score 44; DB 2; Length 269;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLTRKRGK 9
Db 217 RLTRKRGK 225

RESULT 2

S32802
apolipoprotein B - crab-eating macaque (fragment)
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S32802
R:Pape, M.E.; Castle, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.E.; Marotti, K.R.; Melchio
Biochim. Biophys. Acta 1086, 326-334, 1991
A:Title: Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional re
A:Reference number: S32802; MUID:92075708; PMID:1742325
A:Accession: S32802
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-596 <PAP>
A:Cross-references: UNIPROT:Q28473; EMBL:X15737; NID:G38047; PIDN:CAA33755.1; PID:G930124
C:Superfamily: apolipoprotein B

Query Match 100.0%; Score 44; DB 2; Length 596;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLTRKRGK 9
Db 227 RLTRKRGK 235

RESULT 3

JH0102

apolipoprotein B - golden hamster (fragment)

C:Species: Mesocricetus auratus (golden hamster)

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #ext_change 09-Jul-2004

C:Accession: JH0102

R:Smith, T.J.

submitted to GenBank, June 1990

A:Reference number: A38864

A:Accession: JH0102

A:Molecule type: DNA

A:Residues: 1-779 <SMT>

A:Cross-references: UNIPROT:Q60536; GB:M35187

A:Note: this is a revision to the sequence from reference JH0101

Gene 87, 309-310, 1990

A:Title: Sequence of the putative low-density lipoprotein receptor-binding regions of ap

A:Contents: annotation

A:Note: this sequence has been revised in reference A38864

C:Genetics:

A:Gene: apob

C:Superfamily: apolipoprotein B

C:Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;

F:435-443/Region: receptor binding

F:46-656/Region: receptor binding

Query Match

Best Local Similarity 100.0%; Score 44; DB 2; Length 779;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RLRKRGK 9

Db 643 RLTKRGK 651

RESULT 4

LPHUB

apolipoprotein B-100 precursor - human

N:Contains: apolipoprotein B-26; apolipoprotein B-48; apolipoprotein B-74

C:Species: Homo sapiens (man)

C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #ext_change 09-Jul-2004

C:Accession: A27850; A25679; A25263; A25266; A24320; A24684; A2817; A25774; A26

R:Udvardy, E.H.; Blackhart, B.D.; Pletcott, V.R.; Calati, L.; Portier, C.; Knott, T.; Soc

DNA 6, 363-372, 1987

A:Title: DNA sequence of the human apolipoprotein B gene.

A:Reference number: A27850; MUID:88003974; PMID:3652807

A:Accession: A27850

A:Molecule type: DNA

A:Residues: 1-617, 'A', 619-1929, 'F', 1931-3318, 'D', 3320-3426, 'T', 3428-3431, 'O', 3433-3731, 'E', 3733-3734, 'C', 3736-3737, 'M', 3739-3740, 'U', 3742-3743, 'U', 3745-3746, 'U', 3748-3749, 'U', 3751-3752, 'U', 3754-3755, 'U', 3757-3758, 'U', 3760-3761, 'U', 3763-3764, 'U', 3766-3767, 'U', 3769-3770, 'U', 3772-3773, 'U', 3775-3776, 'U', 3778-3779, 'U', 3781-3782, 'U', 3784-3785, 'U', 3787-3788, 'U', 3790-3791, 'U', 3793-3794, 'U', 3796-3797, 'U', 3799-3800, 'U', 3802-3803, 'U', 3805-3806, 'U', 3808-3809, 'U', 3811-3812, 'U', 3814-3815, 'U', 3817-3818, 'U', 3820-3821, 'U', 3823-3824, 'U', 3826-3827, 'U', 3829-3830, 'U', 3832-3833, 'U', 3835-3836, 'U', 3838-3839, 'U', 3841-3842, 'U', 3844-3845, 'U', 3847-3848, 'U', 3850-3851, 'U', 3853-3854, 'U', 3856-3857, 'U', 3859-3860, 'U', 3862-3863, 'U', 3865-3866, 'U', 3868-3869, 'U', 3871-3872, 'U', 3874-3875, 'U', 3877-3878, 'U', 3880-3881, 'U', 3883-3884, 'U', 3886-3887, 'U', 3889-3890, 'U', 3892-3893, 'U', 3895-3896, 'U', 3898-3899, 'U', 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A:Accession: A25572
 A:Molecule type: mRNA
 A:Residues: 4219-4337, 'S', 4339-4563 <PRI>
 A:Cross-references: GB:M36676
 R:Wei, C.F.; Chen, S.H.; Yang, C.Y.; Marcel, Y.L.; Milne, R.W.; Li, W.H.; Sparrow, J.T.;
 Proc. Natl. Acad. Sci. U.S.A. 82, 7265-7269, 1985
 A:Reference number: A24738; MUID:86042646; PMID:2932736
 A:Accession: A24738
 A:Molecule type: mRNA
 A:Residues: 'N', 3729-3731, 'I', 3733-3875, 'A', 3877-3948, 'F', 3950-3963, 'Y', 3965-3982, 'S', 39
 A:Cross-references: GB:M12413; MUID:9178735; PIDN:AA51742.1; PID:9178736
 R:Chen, S.H.; Hahli, G.; Yang, C.Y.; Gu, Z.W.; Lee, B.R.; Weng, S.; Silbermann, S.R.; Cal
 Science 238, 363-366, 1987
 A:Title: Apolipoprotein B-48 is the product of a messenger RNA with an organ-specific in
 A:Reference number: A40133; MUID:88018019; PMID:3659919
 A:Accession: B40133
 A:Molecule type: mRNA
 A:Residues: 2165-2179 <CH>
 A:Cross-references: GB:M18036; PIDN:AA51754.1; PID:9178800
 A:Note: this mRNA includes the stop codon of the organ-specific mRNA for apo48
 A:Accession: A40133
 A:Molecule type: protein
 A:Residues: 51-75; 101-110; 129-139; 158-174; 197-207; 276-287; 298-304; 306-314; 526-532; 538-55
 36; 1486-1498; 1537-1556; 1563-1572; 1601-1610; 1647-1661; 1697-1724; 1770-1781; 1859-1897; 1968-
 A:Note: these fragments were derived from apo48
 R:Hardman, D.A.; Procter, A.A.; Schilling, J.W.; Kane, J.P.
 Biochem. Biophys. Res. Commun. 149, 1214-1219, 1987
 A:Title: Carboxyl terminal analysis of human B-48 protein confirms the novel mechanism f
 A:Reference number: A28002; MUID:88106542; PMID:3426612
 A:Accession: A28002
 A:Molecule type: mRNA
 A:Residues: 2129-2179, 2181-2235 <HA2>
 A:Cross-references: GB:M18471
 A:Experimental source: intestine
 A:Note: this mRNA from intestine includes a stop codon created by RNA editing in place o
 R:Mehrabian, M.; Schumaker, V.N.; Fareed, G.C.; West, R.; Johnson, D.F.; Kirchgessner, T
 Nucleic Acids Res. 13, 6937-6953, 1985
 A:Title: Human apolipoprotein B: identification of cDNA clones and characterization of t
 A:Reference number: A24269; MUID:86041888; PMID:3903660
 A:Accession: A24269
 A:Molecule type: mRNA
 A:Residues: 3056-3159 <MEH>
 A:Cross-references: GB:X03045; NID:G28783; PIDN:CAA26850.1; PID:929609
 R:Hospatankar, A.V.; Higuchi, K.; Law, S.W.; Wehlin, N.; Brewer Jr., H.B.
 Biochem. Biophys. Res. Commun. 148, 279-285, 1987
 A:Title: Identification of a novel in-frame translational stop codon in human intestine
 A:Reference number: A29659; MUID:88049670; PMID:2445342
 A:Accession: A29659
 A:Molecule type: mRNA
 A:Residues: 2169-2179 <HOS>
 A:Note: the sequence shown represents the carboxyl end of apolipoprotein B-48
 A:Note: two RNA species, 14.1kb and 7.5kb in length, were isolated from the human intest
 ch encodes the 250K apoB-48, CAA encoding 2180-Gln is substituted by the stop codon TAA,
 R:Yang, C.; Kim, T.W.; Weng, S.; Lee, B.; Yang, M.; Gotto Jr., A.M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 5523-5527, 1990
 A:Title: Isolation and characterization of sulfhydryl and disulfide peptides of human ap
 A:Reference number: A3783; MUID:90319144; PMID:2115173
 A:Accession: A3783
 A:Contents: disulfide bonds
 A:Molecule type: protein
 A:Residues: 28-41; 76-97, 'I', 99-100; 175-193; 206-215; 239-249; 259-266; 357-399; 455-490; 512-5
 A:Note: cysteines at positions 112, 1422, 1505, 1662, 3761, 3917, and 4217 have free su
 R:Lehoucq, R.C.; Miller, C.; Shively, J.E.; Schumaker, V.N.; Balla, M.A.; Lusis, A.J.
 FEBS Lett. 170, 105-108, 1984
 A:Title: Human apolipoprotein B: partial amino acid sequence.
 A:Reference number: A22006; MUID:84208786; PMID:6373369
 A:Accession: A22006
 A:Molecule type: protein
 A:Residues: 873-892, 'K', 894-896 <LE1>
 A:Accession: B22006
 A:Molecule type: protein
 A:Residues: 3113, 'L', 3115-3130, 'R', 3132-3133, 'P', 3135-3136, 'R' <LE2>

R:Blackhart, B.D.; Ludwig, E.M.; Pierotti, V.R.; Caiati, L.; Onasch, M.A.; Wallis, S.C.;
 U. Biol. Chem. 261, 15364-15367, 1986
 A:Title: Structure of the human apolipoprotein B gene.
 A:Reference number: A92564; MUID:87057153; PMID:2946672
 A:Contents: annotation; gene structure
 R:Wagener, R.; Pfizner, R.; Stofel, W.
 Biol. Chem. Hoppe-Seyler 368, 419-425, 1987
 A:Title: Studies on the organization of the human apolipoprotein B 100 gene.
 A:Reference number: A90715; MUID:87271140; PMID:2886136
 A:Contents: annotation; gene structure
 R:Weisgraber, K.H.; Rall Jr., S.C.
 J. Biol. Chem. 262, 11097-11103, 1987
 A:Title: Human apolipoprotein B-100 heparin-binding sites.
 A:Reference number: A92605; MUID:87280197; PMID:3301850
 A:Contents: annotation; heparin binding and disulfide bond
 R:Daehli, N.; Lee, D.M.; Mok, T.
 Biochem. Biophys. Res. Commun. 137, 493-499, 1986
 A:Title: Apolipoprotein B is a calcium binding protein.
 A:Reference number: A90125; MUID:86242245; PMID:3087360
 A:Contents: annotation; calcium binding
 R:Carlsson, P.; Olafsson, S.O.; Bondjers, G.; Darnfors, C.; Wiklund, O.; Bjurell, G.
 Nucleic Acids Res. 13, 8813-8826, 1985
 A:Title: Molecular cloning of human apolipoprotein B cDNA.
 A:Reference number: 137178; MUID:86093680; PMID:3841204
 A:Accession: 137180
 Query Match 100.0%; Score 44; DB 1; Length 4563;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 LTRRRGK 9
 3386 LTRRRGK 3394
 RESULT 5
 apolipoprotein B-100 - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 31-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
 C:Accession: A60950
 R:Law, A.; Scott, J.
 J. Lipid Res. 31, 1109-1120, 1990
 A:Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL
 A:Reference number: A60950; MUID:90324804; PMID:2373961
 A:Accession: A60950
 A:Molecule type: mRNA
 A:Residues: 1-274 <LAW>
 A:Cross-references: UNIPROT:Q7M2U9
 A:Note: authors translated the codon GAT for residue 155 as His
 C:Superfamily: apolipoprotein B
 C:Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
 Query Match 88.6%; Score 39; DB 2; Length 274;
 Best Local Similarity 100.0%; Pred. No. 2.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 2 LTRRRGK 9
 223 LTRRRGK 230
 RESULT 6
 E60950
 apolipoprotein B-100 - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C:Accession: E60950
 R:Law, A.; Scott, J.
 J. Lipid Res. 31, 1109-1120, 1990
 A:Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL
 A:Reference number: A60950; MUID:90324804; PMID:2373961
 A:Accession: E60950

A/Molecule type: mRNA
A/Residues: 1-275 <LAM>
A/Cross-references: UNIPROT:Q7L277
C/Superfamily: apolipoprotein B
C/Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
Query Match 88.6%; Score 39; DB 2; Length 275;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 223 RLRKRGK 9
223 RLRKRGK 230
RESULT 7
UH0101
apolipoprotein B-100 - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
R/Smith, T.J.; Hautamaa, D.; Maeda, N.
Gene 87, 309-310, 1990
A/Title: Sequence of the putative low-density lipoprotein receptor-binding regions of ap
A/Reference number: JH0101; MWID:9026327; PMID:233175
A/Accession: JH0101
A/Molecule type: DNA
A/Residues: 1-784 <SMI>
A/Cross-references: UNIPROT:Q61314; GB:M35186
R/Smith, T.; Hautamaa, D.; Maeda, N.
Submitted to the EMBL Data Library, May 1989
A/Reference number: S33128
A/Accession: S33128
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-531, 'S', 533-784 <SM2>
A/Cross-references: EMBL:X15191
R/Law, A.; Scott, J.
J. Lipid Res. 31, 1109-1120, 1990
A/Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL
A/Reference number: A60950; MWID:90324804; PMID:2373961
A/Accession: D60950
A/Molecule type: mRNA
A/Residues: 427-531, 'S', 533-700 <LAM>
C/Genetics:
A/Gene: MGI:Apob
A/Cross-references: MGI:88052
C/Superfamily: apolipoprotein B
C/Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
F/435-445/Region: receptor binding
F/646-656/Region: receptor binding
Query Match 86.4%; Score 38; DB 2; Length 784;
Best Local Similarity 88.9%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 648 RLRKRGK 9
1 RLRKRGK 9
648 RLRKRGK 656
RESULT 8
AB1875
hypothetical protein alr0547 [imported] - Nostoc sp. (strain PCC 7120)
C/Species: Nostoc sp. PCC 7120
A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
R/Accession: AB1875
R/Kaneke, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuch
DNA Res. 8, 205-213, 2001
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A/Reference number: AB1807; MWID:21595285; PMID:1175840

A/Accession: AB1875
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-680 <KUR>
A/Cross-references: UNIPROT:Q8YZD0; GB:BA000019; PIDN:BA072505.1; PID:G17129892; GSPDB
C/Genetics:
A/Gene: alr0547
C/Superfamily: hypothetical protein s111033; conserved hypothetical protein y100 homolo
Query Match 84.1%; Score 37; DB 2; Length 680;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Db 544 RVRKRGK 9
1 RVRKRGK 9
544 RVRKRGK 552
RESULT 9
A75334
[acyl-carrier-protein] S-malonyltransferase (EC 2.3.1.39) DR1945 [similarity] - Deinoco
C/Species: Deinococcus radiodurans
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
'M.; Shen, M.; Vamathevan, J.; J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, U.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A/Reference number: A75250; MWID:20036896; PMID:10567266
A/Accession: A75334
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-305 <WHI>
A/Cross-references: UNIPROT:Q9RT24; GB:AB002033; GB:AB000513; NID:G6459726; PIDN:AAF149
A/Experimental source: strain R1
C/Genetics:
A/Gene: DR1945
A/Map position: 1
C/Superfamily: [acyl-carrier-protein] S-malonyltransferase; [acyl-carrier-protein] S-mal
C/Keywords: acyltransferase; coenzyme A
F/7-286/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
F/93/Active site: Ser (covalent substrate-binding) #status predicted
F/198/Active site: His #status predicted
Query Match 79.5%; Score 35; DB 2; Length 305;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 113 RLRKRG 7
1 RLRKRG 7
113 RLRKRG 119
RESULT 10
S34191
sulfite reductase (NADPH2) (EC 1.8.1.2) hemoprotein - Thiocapsa roseopersicina
C/Species: Thiocapsa roseopersicina
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-May-2004
R/Haverkamp, T.; Gieselmann, G.; Schwenn, J.D.
Submitted to the EMBL Data Library, July 1993
A/Description: Structure and function of genes involved in the metabolism of sulfite from
A/Reference number: S34190
A/Accession: S34191
A/Molecule type: DNA
A/Residues: 1-561 <HAV>
A/Cross-references: EMBL:Z23169
C/Superfamily: sulfite reductase
C/Keywords: 4Fe-4S; chromoprotein; cysteine biosynthesis; heme; iron; iron-sulfur protein
F/423-429, 468, 472/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
F/472/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 77.3%; Score 34; DB 1; Length 561;
Best Local Similarity 87.5%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RLTRRGGL 8
|||
Db 449 RLTRRGGL 456

RESULT 11

salivary glue protein homolog precursor - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: S12607
R:Enzyme: M.; Digestion: F.A.; Arriaco, D.; Giordano, E.; Polito, L.C.
Nucleic Acids Res. 18, 5837-5841, 1990
A:Title: A new gene nested within the dunce genetic unit of *Drosophila melanogaster*.
A:Reference number: S12607; MUID:91016924; PMID:2120680
A:Accession: S12607
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-107 <FUR>
A:Cross-references: UNIPROT:P29338; GB:X52118; NID:G394803; PIDN:CAA36363.1; PID:G394804
C:Genetics:
A:Gene: FlyBase:ngl
A:Cross-references: FlyBase:FBgn0002933
A:Map position: 3C11-12
C:Keywords: salivary gland; tandem repeat
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-107/Product: salivary glue protein homolog #status predicted <MAT>
F:31-62/Region: 8-residue repeats

Query Match 75.0%; Score 33; DB 2; Length 107;
Best Local Similarity 55.6%; Pred. No. 20;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLTRRGGL 9
|||
Db 90 RLTRRGGL 98

RESULT 12

salivary glue protein ng-2 - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S33822
R:Enzyme: M.; Digestion: P.P.; Crisp, S.; Attiaco, D.; Polito, L.C.
J. Mol. Biol. 231, 531-538, 1993
A:Title: Dense cluster of genes is located at the ecdysone-regulated 3C puff of *Drosophila*.
A:Reference number: S33822; MUID:93287124; PMID:8510164
A:Accession: S33822
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-112 <FUR>
A:Cross-references: UNIPROT:P40139; EMBL:X61945; NID:G296040; PIDN:CAA43951.1; PID:G2960
C:Genetics:
A:Gene: FlyBase:ng2
A:Cross-references: FlyBase:FBgn0010294

Query Match 75.0%; Score 33; DB 2; Length 112;
Best Local Similarity 55.6%; Pred. No. 21;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLTRRGGL 9
|||
Db 90 RLTRRGGL 98

RESULT 13

T41529

hypothetical protein SPCC645.12c - fission yeast (*Schizosaccharomyces pombe*)
C:Species: *Schizosaccharomyces pombe*
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T41529
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, March 1999
A:Reference number: Z22000
A:Accession: T41529
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-198 <MOO>
A:Cross-references: UNIPROT:Q9Y7V1; EMBL:AL049498; PIDN:CAB39908.1; GSPDB:GN00068; SPDB:
C:Genetics:
A:Gene: SPDB:SPCC645.12c
A:Map position: 3

Query Match 75.0%; Score 33; DB 2; Length 198;
Best Local Similarity 77.8%; Pred. No. 34;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RLTRRGGL 9
|||
Db 15 RLTRRGGL 23

RESULT 14

B69407
M0188 homolog - *Archaeoglobus fulgidus*
N:Alternate names: inosine monophosphate dehydrogenase homolog [misnomer]
C:Species: *Archaeoglobus fulgidus*
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: B69407
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
J. Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glock, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Attiaco, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Weese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo-
A:Reference number: B69250; MUID:98049343; PMID:9389475
A:Accession: B69407
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-259 <KLE>
A:Cross-references: UNIPROT:O29009; GB:AE001017; GB:AE000782; NID:G2689340; PIDN:AAB8998
C:Superfamily: conserved hypothetical protein M0188; CBS homology
F:12-60/Domain: CBS homology <CBS1>
F:71-119/Domain: CBS homology <CBS2>

Query Match 75.0%; Score 33; DB 1; Length 259;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RLTRRGGL 9
|||
Db 227 RLTRRGGL 235

RESULT 15

AH0906
conserved hypothetical protein STY3508 [imported] - *Salmonella enterica* subsp. *enterica*.
C:Species: *Salmonella enterica* subsp. *enterica* serovar Typh
A>Note: this species has also been called *Salmonella typhi*
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AH0906
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Mout, S.; O'Garra, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov-
A:Reference number: AB0502; MUID:21534947; PMID:11677608

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us-10-657-404a-8.rpr

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A/Accession: AH0906
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-309 <PAR>
A/Cross-references: GB:AL513382; PIDN:CMD07846.1; PTD:G16504394; GSPDB:GN0176
C/Genetics:
A/Gene: STY3508
A/Superfamily: Methanococcus jamaashii
A/Superfamily: Methanococcus jamaashii

Query Match	75.0%	Score 33;	DB 2;	Length 309;
Best Local Similarity	66.7%	Pred. No. 51;		
Matches	6;	Conservative	2;	Mismatches 1;

QY	1	RLTRKRGK	9
		: :	
Db	171	RIARERGK	179

Search completed: January 12, 2005, 13:31:58
Job time : 17.5484 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2005, 12:49:11 ; Search time 89.7097 Seconds
(without alignments)
57.724 Million cell updates/sec

Title: US-10-657-404a-8
Perfect score: 44
Sequence: 1 RLTKRGGLK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	414	2	Q7YQ85
2	44	100.0	421	2	Q7TN68
3	44	100.0	432	2	Q7YR10
4	44	100.0	436	2	Q7YQ86
5	44	100.0	438	2	Q7YQ87
6	44	100.0	438	2	Q7YR04
7	44	100.0	445	2	Q7YR08
8	44	100.0	445	2	Q7TN64
9	44	100.0	445	2	Q7TN71
10	44	100.0	445	2	Q7TN72
11	44	100.0	596	2	Q28473
12	44	100.0	780	2	Q60536
13	44	100.0	780	2	Q60537
14	44	100.0	3262	2	Q13788
15	44	100.0	4563	1	APB_HUMAN
16	44	100.0	4563	1	Q72600
17	44	100.0	4563	2	Q72600
18	41	93.2	407	2	Q7TN65
19	41	93.2	412	2	Q7TN69
20	39	88.6	263	2	Q7YQ00
21	39	88.6	274	2	Q7YQ01
22	39	88.6	275	2	Q7YQ02
23	39	88.6	304	2	Q7YQ03
24	39	88.6	314	2	Q7YQ04
25	39	88.6	316	2	Q7YQ05
26	39	88.6	318	2	Q7YQ06
27	39	88.6	319	2	Q7YQ07
28	39	88.6	319	2	Q7YQ08
29	39	88.6	320	2	Q7YQ09
30	39	88.6	322	2	Q7YQ10
31	39	88.6	339	2	Q7YR05

32	39	88.6	361	2	Q7YQ88	Q7YQ88 amblygonus
33	39	88.6	364	2	Q7YQ01	Q7YQ01 dugong dugong
34	39	88.6	386	2	Q7YQ01	Q7YQ01 tupia cana
35	39	88.6	387	2	Q7YQ02	Q7YQ02 phalanger o
36	39	88.6	392	2	Q7YR11	Q7YR11 tarsius byr
37	39	88.6	400	2	Q7YQ09	Q7YQ09 ornithorhyn
38	39	88.6	405	2	Q7YQ00	Q7YQ00 tachyglossu
39	39	88.6	411	2	Q7YQ07	Q7YQ07 octodon pr
40	39	88.6	422	2	Q7YR12	Q7YR12 talpa europ
41	39	88.6	423	2	Q7YQ09	Q7YQ09 sorex monti
42	39	88.6	426	2	Q7YQ02	Q7YQ02 alces alces
43	39	88.6	429	2	Q7YQ08	Q7YQ08 crocidura f
44	39	88.6	438	2	Q7YQ04	Q7YQ04 balana mys
45	39	88.6	440	2	Q7YQ04	Q7YQ04 myotis veli

ALIGNMENTS

```

RESULT 1
Q7YQ85 PRELIMINARY; PRT; 414 AA.
AC Q7YQ85;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Apolipoprotein B 100 (Fragment).
GN Name=apob-100;
OS Aotus vociferans (Spix's owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57176;
RN [1]
RX MEDLINE=22761261; PubMed=12878460;
RA Amling-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
RT "A new phylogenetic marker, apolipoprotein B, provides compelling
RT evidence for eutherian relationships."
DR EMBL; AF548396; AAP97352.1; -.
KW Lipoprotein.
FT NON TER 1 1
FT SEQUENCE 414 AA; 45955 MW; EEP8492157E1BDE CRC64;
SQ
Query Match 100.0%; Score 44; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLTKRGGLK 9
Db 259 RLTKRGGLK 267

RESULT 2
Q7TN68 PRELIMINARY; PRT; 421 AA.
AC Q7TN68;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Apolipoprotein B (Fragment).
OS Glucosylated volans (Southern flying squirrel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Petauriidae;
OC Glucosylated.
OX NCBI_TaxID=64683;
RN [1]
RX MEDLINE=22761261; PubMed=12878460;
RA Amling-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
RT "A new phylogenetic marker, apolipoprotein B, provides compelling
RT evidence for eutherian relationships."

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RL Mol. Phylogenet. Evol. 28:225-240(2003).
DR EMBL; AY24379; AAP50767.1; -.
KW Lipoprotein.
FT NON_TER 1
SQ SEQUENCE 421 AA; 46747 MW; D47B7BD4F64FD1 CRC64;

Query Match 100.0%; Score 44; DB 2; Length 421;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLTRKRGK 9
Db 265 RLTRKRGK 273

RESULT 3

ID QYR10 PRELIMINARY; PRT; 432 AA.
AC QYR10;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DE Apolipoprotein B (Fragment).
OS Diceros bicornis (Black rhinoceros).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Perissodactyla; Rhinocerotidae; Diceros.
OK NCBI_TaxID=9805;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=22761261; PubMed=12878460;
RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
RT "A new phylogenetic marker, apolipoprotein B, provides compelling
RL Mol. Phylogenet. Evol. 28:225-240(2003).
DR EMBL; AY24375; AAP50763.1; -.
KW Lipoprotein.
FT NON_TER 1
SQ SEQUENCE 432 AA; 48171 MW; F27B7AB39604732C CRC64;

Query Match 100.0%; Score 44; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLTRKRGK 9
Db 276 RLTRKRGK 284

RESULT 4

ID QYOM8 PRELIMINARY; PRT; 436 AA.
AC QYOM8;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DE Apolipoprotein B 100 (Fragment).
GN Name-apob-100;
OS Nyctimene albigenter (Common tube-nosed fruit bat).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Chiroptera; Megachiroptera; Pteropodidae;
OK NCBI_TaxID=48988;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=22761261; PubMed=12878460;
RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
RT "A new phylogenetic marker, apolipoprotein B, provides compelling
RL Mol. Phylogenet. Evol. 28:225-240(2003).
DR EMBL; AF548435; AAP97391.1; -.
KW Lipoprotein.

FT NON_TER 1
SQ SEQUENCE 436 AA; 48717 MW; 1C4A7EAD72D2C629 CRC64;

Query Match 100.0%; Score 44; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLTRKRGK 9
Db 280 RLTRKRGK 288

RESULT 5

ID QYOM7 PRELIMINARY; PRT; 438 AA.
AC QYOM7;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DE Apolipoprotein B 100 (Fragment).
GN Name-apob-100;
OS Pteropus hypomelanus (Small flying fox).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Chiroptera; Megachiroptera; Pteropodidae;
OK NCBI_TaxID=9405;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=22761261; PubMed=12878460;
RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
RT "A new phylogenetic marker, apolipoprotein B, provides compelling
RL Mol. Phylogenet. Evol. 28:225-240(2003).
DR EMBL; AF548436; AAP97392.1; -.
KW Lipoprotein.
FT NON_TER 1
SQ SEQUENCE 438 AA; 48734 MW; 2BD5BCB4E2CC41 CRC64;

Query Match 100.0%; Score 44; DB 2; Length 438;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLTRKRGK 9
Db 282 RLTRKRGK 290

RESULT 6

ID QYR04 PRELIMINARY; PRT; 438 AA.
AC QYR04;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DE Apolipoprotein B (Fragment).
OS Roussetus amplexicaudatus (Common roussette).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Chiroptera; Megachiroptera; Pteropodidae;
OK NCBI_TaxID=58083;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=22761261; PubMed=12878460;
RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
RT "A new phylogenetic marker, apolipoprotein B, provides compelling
RL Mol. Phylogenet. Evol. 28:225-240(2003).
DR EMBL; AY24383; AAP50771.1; -.
KW Lipoprotein.
FT NON_TER 1
SQ SEQUENCE 438 AA; 48734 MW; 2BD5BCB4E2CC41 CRC64;

SQ SEQUENCE 438 AA; 48597 MW; 41C890DEAF95C872 CRC64;

Query Match 100.0%; Score 44; DB 2; Length 438;

Best Local Similarity 100.0%; Pred. No. 1.5;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RUTRRKGLK 9
|||||
DB 282 RUTRRKGLK 290

RESULT 7

ID Q7NR08 PRELIMINARY; PRT; 445 AA.

AC Q7NR08: 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE Apolipoprotein B (Fragment).
OS Chaetophractus villosus (South American armadillo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Dasypodidae; Chaetophractus.
OX NCBI_TaxID=29080;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22761261; PubMed=12878460;
RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
RT "A new phylogenetic marker, apolipoprotein B, provides compelling
evidence for eutherian relationships.";
RL Mol. Phylogenet. Evol. 28:225-240(2003).
DR EMBL; AY243378; AAP50766.1; -.
KW Lipoprotein.
FT NON_TER 1
FT NON_TER 445
SQ SEQUENCE 445 AA; 49564 MW; 2DA5DC3ED2F0FDD2 CRC64;

Query Match 100.0%; Score 44; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RUTRRKGLK 9
|||||
DB 289 RUTRRKGLK 297

RESULT 8

ID Q7TN64 PRELIMINARY; PRT; 445 AA.

AC Q7TN64: 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE Apolipoprotein B (Fragment).
GN Name=apob-100;
OS Agouti paca (Paca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Agoutidae; Agouti.
OX NCBI_TaxID=108852;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22761261; PubMed=12878460;
RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
RT "A new phylogenetic marker, apolipoprotein B, provides compelling
evidence for eutherian relationships.";
RL Mol. Phylogenet. Evol. 28:225-240(2003).
DR EMBL; AF548417; AAP97373.1; -.
KW Lipoprotein.
FT NON_TER 1
FT NON_TER 445
SQ SEQUENCE 445 AA; 49721 MW; 34AF7ABE90F121EF CRC64;

Query Match 100.0%; Score 44; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.5;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RUTRRKGLK 9
|||||
DB 289 RUTRRKGLK 297

RESULT 9

ID Q7TN71 PRELIMINARY; PRT; 445 AA.

AC Q7TN71: 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
OS Hydrochoerus hydrochaeris (Capybara) (Carpincho).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Hydrochaeridae;
OC Hydrochaeris.
OX NCBI_TaxID=10149;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22761261; PubMed=12878460;
RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
RT "A new phylogenetic marker, apolipoprotein B, provides compelling
evidence for eutherian relationships.";
RL Mol. Phylogenet. Evol. 28:225-240(2003).
DR EMBL; AY243369; AAP50757.1; -.
DR InterPro; IPR000871; Beta_lactamase_A.
DR PROSITE; PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
KW Lipoprotein.
FT NON_TER 1
FT NON_TER 445
SQ SEQUENCE 445 AA; 49520 MW; CBBA2DD53D7A18D2 CRC64;

Query Match 100.0%; Score 44; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RUTRRKGLK 9
|||||
DB 289 RUTRRKGLK 297

RESULT 10

ID Q7TN72 PRELIMINARY; PRT; 445 AA.

AC Q7TN72: 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE Apolipoprotein B (Fragment).
OS Erethizon dorsatum (North American porcupine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Erethizontidae;
OC Erethizon.
OX NCBI_TaxID=34844;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22761261; PubMed=12878460;
RA Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
RT "A new phylogenetic marker, apolipoprotein B, provides compelling
evidence for eutherian relationships.";
RL Mol. Phylogenet. Evol. 28:225-240(2003).
DR EMBL; AY243368; AAP50756.1; -.
KW Lipoprotein.
FT NON_TER 1
FT NON_TER 445
SQ SEQUENCE 445 AA; 49617 MW; 9572FE5FE7625F2 CRC64;

Query Match 100.0%; Score 44; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLTRKRGK 9
Db 289 RLTRKRGK 297

RESULT 11

Q28473 ID Q28473 PRELIMINARY; PRT; 596 AA.
AC Q28473; 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DE 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
OS Apolipoprotein B (Fragment).
OC Macaca fascicularis (Cebus eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=92075708; PubMed=1742325;
RA Page M.E., Castle C.K., Murray R.W., Funk G.M., Hunt C.E.,
RA Macotri K.R., Melchior G.W.,
RA "Apo B metabolism in the cynomolgus monkey: evidence for post-
transcriptional regulation.";
RL Biochim. Biophys. Acta 1086:326-334(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Murray R.;
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; X15737; CAA33755.1; -.
KW Lipoprotein.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 596 AA; 66757 MW; B13BA74E25C3120 CRC64;
Query Match 100.0%; Score 44; DB 2; Length 596;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12

Q60536 ID Q60536 PRELIMINARY; PRT; 780 AA.
AC Q60536; 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DE 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
OS Mesocricetus auratus (Golden hamster).
OC Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=90236327; PubMed=2332175;
RA Smith T.J., Hautamaa D., Maeda N.;
RA "Sequence of the putative low-density lipoprotein receptor-binding
regions of apolipoprotein B in mouse and hamster.";
RL Gene 87:309-310(1990).
DR EMBL; M35187; AAA37059.1; -.
DR PIR; C60950; C60950.
DR PIR; JH0102; JH0102.
KW Lipoprotein.

FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 780 AA; 86625 MW; E371D1B2079D8F7E CRC64;
Query Match 100.0%; Score 44; DB 2; Length 780;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLTRKRGK 9
Db 643 RLTRKRGK 651

RESULT 13

Q60537 ID Q60537 PRELIMINARY; PRT; 780 AA.
AC Q60537; 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DE 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
OS Apolipoprotein B (Fragment).
OC Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Smith T., Hautamaa D., Maeda N.;
RL Submitted (MAY-1989) to the EMBL/GenBank/DBJ databases.
DR EMBL; X15192; CAA33266.1; -.
KW Lipoprotein.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 780 AA; 86904 MW; 2D19CEA92170B6F9 CRC64;
Query Match 100.0%; Score 44; DB 2; Length 780;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14

Q13788 ID Q13788 PRELIMINARY; PRT; 3262 AA.
AC Q13788; 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DE 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
OS APOB protein (Fragment).
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=87191999; PubMed=2883086;
RA Carlson P., Darnfore C., Olofsson S.O., Bjurell G.;
RA "Analysis of the human apolipoprotein B gene; complete structure of
the B-74 region.";
RL Gene 49:29-51(1986).
DR EMBL; M15421; AAA51758.1; -.
DR PIR; A27850; LPHUB.
DR GO; GO:0005576; C:extracellular; NMS.
DR GO; GO:0005319; F:lipid transporter activity; NMS.
DR GO; GO:0008689; P:lipid transport; NMS.
FT NON_TER 1

SO SEQUENCE 3262 AA; 370140 MW; 56603BC0618DD40D CRC64;
Query Match 100.0%; Score 44; DB 2; Length 3262;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RLTRRGGLK 9
Db 2085 RLTRRGGLK 2093
RESULT 15
APB_HUMAN STANDARD; PRT; 4563 AA.
ID P04114; 000502; Q13787;
AC 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipoprotein
B-48 (Apo B-48)].
GN Name=APOB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87016385; PubMed=3763409;
RA Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.,
RA Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;
RT "Complete cDNA and derived protein sequence of human apolipoprotein B-
100.";
RT Nucleic Acids Res. 14:7501-7503(1986).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT GLU-4181.
RX MEDLINE=88003974; PubMed=3652907;
RA Ludwig E.H., Blackhart B.D., Pierotti V.R., Caiati L., Fortier C.,
RA Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.;
RT "DNA sequence of the human apolipoprotein B gene.";
RT DNA 6:363-372(1987).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS ILE-98 AND GLU-4181.
RX MEDLINE=87008488; PubMed=3759943;
RA Chen S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,
RA Goto A.M., Jr., Chan L.;
RT "The complete cDNA and amino acid sequence of human apolipoprotein B-
100.";
RT J. Biol. Chem. 261:12918-12921(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=87041416; PubMed=3464946;
RA Law S.W., Grant S.M., Higuchi K., Hospattankar A.V., Lackner K.J.,
RA Lee N., Brewer H.B., Jr.;
RT "Human liver apolipoprotein B-100 cDNA: complete nucleic acid and
RT derived amino acid sequence.";
RT Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146(1986).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=87161758; PubMed=3030729;
RA Cladaras C., Hadjopoulos-Cladaras M., Nolte R.T., Atkinson D.,
RA Zannis V.I.;
RT "The complete sequence and structural analysis of human apolipoprotein
RT B-100: relationship between apoB-100 and apoB-48 forms.";
RL EMO 5:3495-3507(1986).
RN [6]
RP SEQUENCE OF 709-906 FROM N.A.
RX MEDLINE=85270450; PubMed=3860836;
RA Deeb S.S., Motulsky A.G., Alberts J.U.;
RT "A partial cDNA clone for human apolipoprotein B.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986(1985).
RN [7]
RP SEQUENCE OF 3056-3159 FROM N.A.
RX MEDLINE=86041886; PubMed=3903660;

RA Mehrabian M., Schumaker V.N., Fareed G.C., West R., Johnson D.F.,
RA Kirchengastner T.G., Lin H.-C., Wang X., Ma Y., Mendiaz E., Lusis A.J.;
RT "Human apolipoprotein B: identification of cDNA clones and
RT characterization of mRNA.";
RL Nucleic Acids Res. 13:6937-6953(1985).
RN [8]
RP SEQUENCE OF 1937-2018 AND 3811-4334 FROM N.A., AND VARIANT GLU-4181.
RX MEDLINE=86093680; PubMed=3841204;
RA Carlsson P., Olafsson S.O., Bondjere G., Darnfors C., Wiklund O.,
RA Bjursell G.;
RT "Molecular cloning of human apolipoprotein B cDNA.";
RL Nucleic Acids Res. 13:8813-8826(1985).
RN [9]
RP SEQUENCE OF 3109-4563 FROM N.A.
RX MEDLINE=85300528; PubMed=2994225;
RA Knott T.J., Rall S.C., Jr., Innerarity T.L., Jacobson S.F., Urdea M.S.,
RA Levy-Wilson B., Powell L.M., Pease R.J., Eddy R., Nakai H., Byers M.,
RA Priestley L.M., Robertson E., Rall L.B., Betsholtz C., Shown T.B.,
RA Mahley R.W., Scott J.;
RT "Human apolipoprotein B: structure of carboxyl-terminal domains, sites
RT of gene expression, and chromosomal localization.";
RL Science 230:37-43(1985).
RN [10]
RP SEQUENCE OF 1-291 FROM N.A.
RX MEDLINE=86149325; PubMed=3513177;
RA Procter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V.,
RA Chen G.C., Kirsner S.W., McEnroe G., Kane J.P.;
RT "Isolation of a cDNA clone encoding the amino-terminal region of human
RT apolipoprotein B.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:1467-1471(1986).
RN [11]
RP SEQUENCE OF 1-1670 FROM N.A., AND VARIANT ILE-98.
RX MEDLINE=86287319; PubMed=3461454;
RA Procter A.A., Hardman D.A., Sato K.Y., Schilling J.W., Yamanaka M.,
RA Hort Y.J., Hjertild K.A., Chen G.C., Kane J.P.;
RT "Analysis of cDNA clones encoding the entire B-26 region of human
RT apolipoprotein B.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682(1986).
RN [12]
RP PARTIAL SEQUENCE, AND IDENTIFICATION OF APO-B48.
RX MEDLINE=88018019; PubMed=3659919;
RA Chen S.-H., Habib G., Yang C.-H., Gu Z.-W., Lee B.R., Weng S.-H.,
RA Silberman S.R., Cai S.-J., Deslypere J.P., Rosenau M.,
RA Goto A.M., Jr., Li W.-H., Chan L.;
RT "Apolipoprotein B-48 is the product of a messenger RNA with an organ-
RT specific in-frame stop codon.";
RL Science 238:363-366(1987).
RN [13]
RP DOMAINS.
RX MEDLINE=87039351; PubMed=3773997;
RA Knott T.C., Pease R.J., Powell L.M., Wallis S.C., Rall S.C., Jr.,
RA Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R.,
RA Johnson D., Fuller M., Lusis A.J., McCarthy B.J., Mahley R.W.,
RA Levy-Wilson B., Scott J.;
RT "Complete protein sequence and identification of structural domains of
RT human apolipoprotein B.";
RL Nature 323:734-738(1986).
RN [14]
RP DOMAINS.
RX Yang C.-Y., Chen S.-H., Gianturco S.H., Bradley W.A., Sparrow J.T.,
RA Tanimura M., Li W.-H., Sparrow D.A., DeLoof H., Rosenau M.,
RA Lee F.-S., Gu Z.-W., Goto A.M., Jr., Chan L.;
RT "Sequence, structure, receptor-binding domains and internal repeats of
RT human apolipoprotein B-100.";
RL Nature 323:738-742(1986).
RN [15]
RP CALCIUM-BINDING DATA.
RX MEDLINE=86242245; PubMed=3087360;
RA Daehli N., Lee D.M., Mok T.;
RT "Apolipoprotein B is a calcium binding protein.";
RL Biochem. Biophys. Res. Commun. 137:493-499(1986).
RN [16]
RP PALMITOYLATION OF CVS-1112.

RX MEDLINE=20143590; PubMed=10679026;
RA Zhao Y., McCabe J.B., Vance J., Berthiaume L.G.;
RT "Palmitoylation of apolipoprotein B is required for proper
RT intracellular sorting and transport of cholesterol esters and
RL triglycerides.";
RN Mol. Biol. Cell 11:721-734(2000).
RP [17]
RX VARIANT SER-4338.
RA MEDLINE=91071750; PubMed=19793113;
RA Navajas M., Laurent A.-M., Moreel J.-F., Ragab A., Cambou J.-P.,
RA Cuny G., Cambien F., Roizes G.;
RT "Detection by denaturing gradient gel electrophoresis of a new
RL polymorphism in the apolipoprotein B gene.";
RN Hum. Genet. 86:91-93(1990).
RP [18]
RX VARIANT FDB GLN-3527.
RA MEDLINE=89098975; PubMed=2563166;
RA Soria L.F., Ludwig E.H., Clarke H.R.G., Vega G.L., Grundy S.M.,
RA McCarthy B.J.;
RT "Association between a specific apolipoprotein B mutation and familial
RT defective apolipoprotein B-100.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).
RN [19]
RX VARIANT LEU-2739.
RA MEDLINE=91016974; PubMed=2216805;
RA Huang L.-S., Gavish D., Breslow J.L.;
RT "Sequence polymorphism in the human apob gene at position 8344.";
RL Nucleic Acids Res. 18:5922-5922(1990).
RN [20]
RX VARIANT FDB CYS-3558.
RA MEDLINE=95190020; PubMed=7883971;
RA Pullinger C.R., Hennesy L.K., Chatterton J.E., Liu W., Love J.A.,
RA Mendel C.M., Proet P.H., Malloy M.J., Schumaker V.N., Kane J.P.;
RT "Familial ligand-defective apolipoprotein B. Identification of a new
RL mutation that decreases LDL receptor binding affinity.";
RN J. Clin. Invest. 95:1225-1234(1995).
RP [21]
RX VARIANTS LEU-1437; SER-1914; LYS-2566; THR-3121; ALA-3945; MET-4128
RP AND THR-4481.
RX MEDLINE=97044521; PubMed=8889592;
RA Poirier O., Ricard S., Behague I., Souriau C., Evans A.E.,
RA Arveiler D., Marques-Vidal P., Luc G., Roizes G., Cambien F.;
RT "Detection of new variants in the apolipoprotein B (Apo B) gene by
RL PCR-SSCP.";
RN Hum. Mutat. 8:282-285(1996).
RP [22]
RX VARIANTS FDB GLN-3527 AND CYS-3558.
RA MEDLINE=97403938; PubMed=9259199;
RA Rabes J.P., Varret M., Saint-Jore B., Erlich D., Jondeau G.,
RA Kempf M., Giraudet P., Junten C., Boileau C.;
RT "Familial ligand-defective apolipoprotein B-100: simultaneous
RT detection of the ARG3500-->GLN and ARG3531-->CYS mutations in a French
RL Hum. Mutat. 10:160-163(1997).
RN [23]
RX VARIANTS SER-1914; ARG-1923; LEU-2739; ASP-3319; THR-3427; GLN-3432
RP AND ILE-3921.
RX MEDLINE=98141125; PubMed=9490296;
RA Leren T.P., Bakken K.S., Hoel V., Hjermann I., Berg K.;
RT "Screening for mutations of the apolipoprotein B gene causing
RT hypocholesterolemia.";
RL Hum. Genet. 102:44-49(1998).
RP [24]
RX FUNCTION: Apolipoprotein B is a major protein constituent of
CC chylomicrons (apo B-48), LDL (apo B-100) and VLDL (apo B-100). Apo
CC B-100 functions as a recognition signal for the cellular binding
CC and internalization of LDL particles by the apoB/E receptor.
CC [25]
RX -1- SUBCELLULAR LOCATION: Secreted.

Db |||||
3386 RLTRKRGK 3394

Search completed: January 12, 2005, 13:30:54
Job time : 89.7097 secs

Query Match 100.0%; Score 44; DB 1; Length 4563;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RLTRKRGK 9